

1	767	100.0	145	8	AD048473	Ado48473	Rat PTH 1
2	746	97.3	145	8	AD048479	Ado48479	Mouse PTH
3	645	84.1	145	4	AA895018	AA895018	Human prepro
4	645	84.1	145	5	AA019498	AA019498	Hs1 protease
5	645	84.1	145	6	AB858666	AB858666	Human cart
6	645	84.1	145	7	AD031800	AD031800	Human cart
7	645	84.1	145	7	AD046959	AD046959	Human nov
8	645	84.1	145	8	AD048475	AD048475	Human and
9	617.5	80.5	149	7	AD046961	AD046961	Brain and
10	473.5	61.7	149	7	AD046963	AD046963	Brain and
11	335.5	43.7	92	5	AD081902	AD081902	Human dio
12	294	38.3	54	8	AD048481	AD048481	Mouse PTH
13	288	37.5	73	7	AD046962	AD046962	Brain and
14	278	36.2	54	7	AD046960	AD046960	Brain and
15	278	36.2	54	8	AD048477	AD048477	Human PTH
16	272	35.5	80	7	AD046964	AD046964	Brain and
17	140	18.3	25	7	AD046976	AD046976	Brain and
18	99	12.9	18	7	AD046977	AD046977	Brain and
19	92.5	12.1	778	2	AA813456	AA813456	Brain and
20	89	11.6	16	8	AD048482	AD048482	PTH respo
21	87.5	11.4	260	4	ABG09899	ABG09899	Novel hum
22	87.5	11.4	592	4	ABG15607	ABG15607	Novel hum
23	85.5	11.1	274	8	AD0709773	AD0709773	Plant full

Abu117344	Protein e
Ad363688	Acinetob
Aad25502	Stenotro
ADP35524	Fungal Z
Aae14666	S. Glavi
Ad710131	Human he
Aad40296	Human po
Aad40295	Human po
Aam42081	Human po
Aam42082	Human po
Adq89624	Antgonis
Aau31506	Novel hum
ADg213179	Novel hum
ADg151531	Novel hum
Adx739352	Plant wh
Ag8649330	Slrimp wh
Hay00097	Enterococ
ADP431316	F. faecali
ADb483144	F. faecali
ADb313595	Enteroco
Ady318910	Novel Ent
May00096	Enterococ

CC a PAIGB polypeptide; a composition for regulating bone-forming activity

CC In a mammal comprising the nucleic acid fragment, polypeptide or antibody

XX KM Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX OS Homo sapiens.
 XX PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PE 28-JUL-2000; 2000EP-00116126.
 XX PR 29-JUL-1999; 99JP-00248036.
 XX PR 27-AUG-1999; 99JP-00300253.
 XX PR 11-JAN-2000; 2000JP-00118776.
 XX PR 02-MAY-2000; 2000JP-00183767.
 XX PR 09-JUN-2000; 2000JP-00241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Oca T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX DR WPI, 2001-318749/34.
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 XX PS Claim 8; SEQ ID NO 16726; 2537pp + Sequence listing; English.
 XX CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence and 3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
 XX CC Sequence 145 AA;
 XX SQ

Query Match 84.1%; Score 645; DB 4; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1,4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGGSGRADAIERPRYESWTRETSTWLTYYTSDALPSAAATDSGPEAGGIAHAGVLEDGP 60
 DB 1 MCGGSGRADAIERPRYESWTRETSTWLTYYTSDAPPSAAAPDSGPEAGGIAHAGVLEDGL 60
 QY 61 SSGNGVRPAPAGGIANPEKKKNCGTCCPNSSGSLTOKONGLMTTEAKRDAKMSAR 120
 DB 61 PSNGVPRSTAPGGINPEKKKNCGTCCPNSSGSLTOKONGLMTTEAKRDAKMPAK 120
 QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
 DB 121 EVTINVTDSTIQMDRSRRTTKNCVN 145

RESULT 4
 ID AAO19498 standard; protein; 145 AA.
 XX AC AAO19498;
 XX DT 20-DEC-2002 (first entry)
 XX DE Hs1 protein variant.
 XX KM Hs1; variant; cancer; tumour; ungine cluster; cytostatic; metastasis;
 XX KM Bst; expressed sequence tag; colon cancer; stomach cancer; breast cancer;
 XX KM Hs169395; Hs127144; Hs2; Hs132793; Hs3.
 XX OS Unidentified.
 XX PN DE10103694-AL.
 XX PD 01-AUG-2002.
 XX PE 26-JAN-2001; 2001DE-01003694.
 XX PR 26-JAN-2001; 2001DE-01003694.
 XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX PI Bret D, Kemmerer W;
 XX DR WPI; 2002-644836/70.
 XX DR N-PSDB; AAL50100.
 XX PT Diagnosis and therapy of tumors, by determining expression rates of specific expressed sequence tags of the ungine cluster, and subsequently blocking their expression.
 XX PS Claim 10; Page 5; 10pp; German.
 XX CC The present invention relates to the use of expressed sequence tags (ESTs), or variants, of the ungine cluster Hs169395 (Hs1), Hs127144 (Hs2) and/or Hs132793 (Hs3) for diagnosis and therapy of tumors, in which their expression rates in tumour cells and/or lymph nodes are determined. The EST sequences are useful as prognostic markers of survival of cancer patients (high levels of EST-related mRNA are associated with a poor prognosis, specifically correlated with development of metastases); and for diagnosis and/or therapy of solid tumors, particularly of colon, stomach and breast. The present sequence is a variant of the Hs1 protein shown in the exemplification of the present invention.
 XX CC Sequence 145 AA;
 XX SQ

Query Match 84.1%; Score 645; DB 5; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1,4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGGSGRADAIERPRYESWTRETSTWLTYYTSDALPSAAATDSGPEAGGIAHAGVLEDGP 60
 DB 1 MCGGSGRADAIERPRYESWTRETSTWLTYYTSDAPPSAAAPDSGPEAGGIAHAGVLEDGL 60
 QY 61 SSGNGVRPAPAGGIANPEKKKNCGTCCPNSSGSLTOKONGLMTTEAKRDAKMSAR 120
 DB 61 PSNGVPRSTAPGGINPEKKKNCGTCCPNSSGSLTOKONGLMTTEAKRDAKMPAK 120
 QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
 DB 121 EVTINVTDSTIQMDRSRRTTKNCVN 145

RESULT 5
 ID ABR58646 standard; protein; 145 AA.
 XX AC ABR58646;
 XX

XX 09-JUL-2003 (first entry)
 XX Human cancer related protein SEQ ID NO:303.
 DE Human cancer related protein SEQ ID NO:303.
 XX Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KM heart disease; atherosclerosis; endometriosia.
 XX Homo sapiens.
 OS WO2003025138-A2.
 PN 27-MAR-2003.
 PD 17-SEP-2002; 2002WO-US029560.
 XX 17-SEP-2002; 2001US-0323469P.
 PR 20-SEP-2001; 2001US-0323887P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 08-FEB-2002; 2002US-0355145P.
 PR 08-FEB-2002; 2002US-0355257P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
 PI Zlotnick A;
 PI WPI; 2003-354600/33.
 DR N-PSDB; ACC72796.
 XX New genes that are up-regulated or down-regulated in cancers, useful as
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 PT therapeutic targets for screening drugs for treating these diseases.
 XX Claim 12; Page 753; 767pp; English.
 XX The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
 CC related gene nucleotide sequences which encode the proteins given in
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
 CC atherosclerosis and endometriosia. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies
 XX
 SQ Sequence 145 AA:
 Query Match 84.1%; Score 645; DB 6; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1.4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

DB 121 EVTINVTDSIQMDRSRRITKNCVN 145
 |||:::|||||:|||||:
 RESULT 6
 ADC31800
 ID ADC31800 standard; protein, 145 AA.
 XX
 AC ADC31800;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human novel polypeptide sequence, SEQ ID NO:1882.
 XX
 KM Human; diagnostic; drug screening; forensics; gene mapping;
 KM biodiversity assessment; Parkinson's disease; Alzheimer's disease;
 KM neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
 KM ulcers; osteoporosis; autoimmune disease; cancer;
 KM molecular weight marker; food supplement; antiparkinsonian; nootropic;
 KM neuroprotective; antianemic; anticoagulant; thrombolytic; valnerary;
 KM anticancer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
 KM gene therapy; chromosome 8.
 XX Homo sapiens.
 OS
 XX WO2003029271-A2.
 PN 10-APR-2003.
 PD 24-SEP-2002; 2002WO-US030474.
 PF 24-SEP-2002; 2001US-0324631P.
 XX
 PR 24-SEP-2001; 2001US-0324631P.
 XX (HYSE-) HYSEQ INC.
 PA Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
 PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
 PI Haley-Vicente D, Drmanac RT;
 XX
 DR WPI; 2003-371981/35.
 DR N-PSDB; ADC30829.
 XX New polynucleotide and polypeptide useful for diagnosing, preventing or
 PT treating conditions such as neurodegenerative diseases, anemias, platelet
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.
 XX Claim 20; SEQ ID NO 1882; 1185pp; English.
 XX The invention relates to 971 novel human cDNA sequences (ADC29919-
 CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
 CC invention also relates to nucleic acid sequences over 99% identical with
 CC the novel human cDNAs. The invention additionally encompasses expression
 CC vectors and host cells comprising a nucleic acid of the invention; the
 CC recombinant production of a polypeptide of the invention; an antibody
 CC against a polypeptide of the invention; a method of detecting
 CC polynucleotides or polypeptides of the invention; and methods of
 CC identifying a compound which binds to a polypeptide of the invention. The
 CC invention further discloses methods of preventing, treating or
 CC ameliorating a medical condition; kits comprising polynucleotide probes
 CC and/or monoclonal antibodies for carrying out the methods of the
 CC invention; methods for the identification of compounds that modulate the
 CC expression or activity of the polynucleotide and/or polypeptide; and 767
 CC contig sequences corresponding to the cDNA sequences of the invention
 CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
 CC ADC33394). The nucleic acids and polypeptides of the invention are
 CC useful in diagnostics, drug screening, forensics, gene mapping, in the
 CC identification of mutations responsible for genetic disorders or other
 CC traits, for assessing biodiversity, and in producing many other types of
 CC data and products dependent on DNA and amino acid sequences. They are
 CC also used for treating diseases such as Parkinson's disease, Alzheimer's
 CC disease and other neurodegenerative diseases, anaemia, platelet
 CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

CC cancer. The nucleic acids may also be used as hybridization probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human polypeptide sequence of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 145 AA;

Query Match 84.1%; Score 645; DB 7; Length 145;
Best Local Similarity 83.4%; Pred. No. 1,4e-62;

Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIERPYYESWTRTESWLTYYTSDALPSAAATDSGPBAGGHHAGVLEDP 60
DB 1 MCGCGSRADAIERPYYESWTRTESWLTYYTSDALPSAAAPDSGPBAGGHHAGVLEDP 60
QY 61 SSGNVLPAPAGGIANPEKKKNGCTGCPNSOSLSGGPLTKONGLWTEAKRDARKRSAR 120
DB 61 PSNGVPRSTAPGGIPNPEKKTNCCTGCPNPQSLSSGPLTKONGLOTTEAKRDARKMPAK 120
QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
DB 121 EVTINVTDSIQMDRSRRITKNCVN 145

RESULT 7

AD046959
ID ADM46959 standard; protein; 145 AA.

AC ADM46959;

DT 03-JUN-2004 (first entry)

DE Brain and Acute Leukemia, Cytoplasmic alternate protein #1.

XX acute myelogenous leukemia; gene expression; BAALC;

KM chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;

XX Cytoplasmic; exon.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Misc-difference 41 /note= "encoded by GCS"

XX WO2003040347-A2.

XX 15-MAY-2003.

XX 12-NOV-2002; 2002WO-US036375.

XX 09-NOV-2001; 2001US-0348210P.

XX (OHIS) UNIV OHIO STATE RES FOUND.

XX Tanner SM, De la Chapell A;

XX WPI, 2003-441564/41.

XX N-PSDB; ADM46951.

XX Characterizing acute or chronic myelogenous leukemia, or prostate cancer
PT in a patient comprises assaying for the overexpression of one or more
PT BAALC transcripts in cells obtained from the patient.

XX Disclosure; SEQ ID NO 17; 78pp; English.

XX The invention relates to a method of characterizing acute myelogenous

XX leukemia (AML) in a patient by assaying for the overexpression of one or

XX more BAALC transcripts in cells obtained from the patient, where an
CC overexpression indicates that the patient has an aggressive form of AML.

CC The methods, kits and probes are useful for characterizing acute or
CC chronic myelogenous leukemia, or prostate cancer. They are also useful
CC for detecting BAALC overexpression. This sequence corresponds to a BAALC
CC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
CC spliced RNA consisting of exons 1, 6 and 8.

SQ Sequence 145 AA;

Query Match 84.1%; Score 645; DB 7; Length 145;
Best Local Similarity 83.4%; Pred. No. 1,4e-62;

Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIERPYYESWTRTESWLTYYTSDALPSAAATDSGPBAGGHHAGVLEDP 60
DB 1 MCGCGSRADAIERPYYESWTRTESWLTYYTSDALPSAAAPDSGPBAGGHHAGVLEDP 60
QY 61 SSGNVLPAPAGGIANPEKKKNGCTGCPNSOSLSGGPLTKONGLWTEAKRDARKRSAR 120
DB 61 PSNGVPRSTAPGGIPNPEKKTNCCTGCPNPQSLSSGPLTKONGLOTTEAKRDARKMPAK 120
QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
DB 121 EVTINVTDSIQMDRSRRITKNCVN 145

RESULT 8

AD048475
ID ADO48475 standard; protein; 145 AA.

AC ADO48475;

DT 12-AUG-2004 (first entry)

DE Human PTH responsive gene protein.

XX PTH responsive gene; PAlGB, bone-forming; bone; bone density modulation;

KM transgenic animal; osteopathic; gene therapy; osteoporosis; human.

XX Homo sapiens.

XX WO2004044152-A2.

XX 27-MAY-2004.

XX 10-NOV-2003; 2003WO-US035655.

XX 12-NOV-2002; 2002US-0425532P.

XX (AMHP) WYETH.

XX Robinson JA, Stojanovic-Susulic V, Bablj P, Murrills RJ;

XX WPI, 2004-420289/39.

XX N-PSDB; ADO48474.

XX New nucleic acid fragment encoding a PAlGB polypeptide, useful in
PT preparing a composition for diagnosing, treating or preventing bone
PT related disorders, e.g., osteoporosis.

XX Claim 9; SEQ ID NO 4; 169pp; English.

XX The invention relates to a novel PTH responsive gene (PAlGB) fragment
XX encoding a polypeptide. The invention further comprises: a chimeric
XX construct comprising the isolated nucleic acid fragment operatively
XX linked to suitable regulatory sequences; a host cell transformed with the
XX chimeric construct; a vector comprising the nucleic acid fragment;XX obtaining a nucleic acid fragment encoding the polypeptide; a method for
XX fragment; an antibody that specifically binds to one or more epitopes of
XX a PAlGB polypeptide; a composition for regulating bone-forming activity
XX in a mammal comprising the nucleic acid fragment, polypeptide or antibodyXX ; an agent that alters the expression of PAlGB gene or polypeptide;
XX determining whether an agent alters the expression of PAlGB mRNA;

CC screening agents for effectiveness in altering expression of the nucleic
 CC acid fragment; screening for agents useful for treating bone related
 CC disorders; evaluating the efficacy of a treatment of a bone related
 CC disorder in a subject; identifying polypeptides capable of binding to
 CC PAIGB; monitoring the effectiveness of treatment of a subject with a bone
 CC related agent; a transgene animal comprising the DNA; an animal model
 CC for the study of bone density modulation comprising a first group of
 CC animals composed of the transgene animal and a second group of control
 CC animals; studying bone mass determinants; studying the modulation of bone
 CC mass; studying an effect of PAIGB on bone disorders; identifying an agent
 CC for treating bone related disorders; identifying whether an agent which
 CC has bone forming activity; and a stably transfected cell line comprising
 CC two constructs, the first construct comprising a ligand binding domain
 CC linked to a DNA binding domain which is linked to an activation domain
 CC all of which expression is driven by a constitutive promoter, the second
 CC construct comprising multiple copies of DNA binding elements linked to a
 CC minimal promoter which is linked to PAIGB cDNA, where upon the addition
 CC of chemical inducer, transcription of PAIGB gene is induced. The PAIGB
 CC polynucleotide has osteopathic activity. The PTH responsive gene may be
 CC used to treat disorders by gene therapy. The nucleic acid is useful in
 CC preparing a composition for diagnosing, treating or preventing bone
 CC related disorders, e.g., osteoporosis. This sequence represents a PTH
 CC responsive gene protein of the invention.

XX Sequence 145 AA;

Query Match 84.1%; Score 645; DB 8; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1.4e-65;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIIBPYYESWTRTESTWLTYYTSDALPSAAATDSGPAGGLHAGLEDGP 60
 DB 1 MCGCGSRADAIIBPYYESWTRTESTWLTYYTSDAPSAAPDSGPAGGLHSGMLDGL 60
 QY 61 SSGVLRPAAPGAIANEKKMNGCTOCNPSGLTOKONGLTMTTEAKRDAKRSAR 120
 DB 61 PSNGVPRSTAPGGIPNEKKTNCCTCCNPSSLSSGFLTKONGLTTEAKRDAKRPAPK 120
 QY 121 EVAISTENIROMDRSKRVTKNCIN 145
 DB 121 EVTINVTDSIQOMDRSRRTKNCVN 145

RESULT 9

ADM46961
 ID ADM46961 standard; protein; 180 AA.

AC ADM46961;

DT 03-JUN-2004 (first entry)

DE Brain and Acute Leukemia, Cytoplasmic alternate protein #3.

KM acute myelogenous leukemia; gene expression; BAALC;

KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;

KM Cytoplasmic; exon.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 41 /note= "encoded by GCS"

PN WO2003040347-A2.

PD 15-MAY-2003.

PF 12-NOV-2002; 2002WO-US036375.

PR 09-NOV-2001; 2001US-0348210P.

PA (OHIS) UNIV OHIO STATE RES FOUND.

PI Tanner SM, De la Chapell A;
 XX WPI; 2003-441564/41.
 DR N-PSDB; ADM46963.

XX Characterizing acute or chronic myelogenous leukemia, or prostate cancer
 PT in a patient comprises assaying for the overexpression of one or more
 PT BAALC transcripts in cells obtained from the patient.

PS Disclosure; SEQ ID NO 19; 78pp; English.

CC The invention relates to a method of characterizing acute myelogenous
 CC leukemia (AML) in a patient by assaying for the overexpression of one or
 CC more BAALC transcripts in cells obtained from the patient, where an
 CC overexpression indicates that the patient has an aggressive form of AML.
 CC The methods, kits and probes are useful for characterizing acute or
 CC chronic myelogenous leukemia, or prostate cancer. They are also useful
 CC for detecting BAALC overexpression. This sequence corresponds to a BAALC
 CC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
 CC spliced RNA consisting of exons 1, 6 and 8.

XX Sequence 180 AA;

Query Match 80.5%; Score 617.5; DB 7; Length 180;
 Best Local Similarity 67.2%; Pred. No. 2.1e-59;
 Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;

QY 1 MCGCGSRADAIIBPYYESWTRTESTWLTYYTSDALPSAAATDSGPAGGLHAGLEDGP 53
 DB 1 MCGCGSRADAIIBPYYESWTRTESTWLTYYTSDAPSAAPDSGPAGGLHSGMLDGL 60
 QY 54 -----GVLDDGPSNGVLRPAAPGAIANEKKMNGCT 85
 DB 61 KIRAPTVSDEGLFSAKXKAPLAVPSHGMLDGLPSNGVPRSTAPGGINPEKKTNCET 120
 QY 86 QCNPSGLSSGFLTKONGLTTEAKRDAKRSARVAISTENIROMDRSKRVTKNCIN 145
 DB 121 QCNPSGLSSGFLTKONGLTTEAKRDAKRSARVAISTENIROMDRSKRVTKNCIN 180

RESULT 10

ADM46963
 ID ADM46963 standard; protein; 149 AA.

AC ADM46963;

DT 03-JUN-2004 (first entry)

DE Brain and Acute Leukemia, Cytoplasmic alternate protein #5.

KM acute myelogenous leukemia; gene expression; BAALC;

KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;

KM Cytoplasmic; exon.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 41 /note= "encoded by GCS"

PN WO2003040347-A2.

PD 15-MAY-2003.

PF 12-NOV-2002; 2002WO-US036375.

PR 09-NOV-2001; 2001US-0348210P.

PA (OHIS) UNIV OHIO STATE RES FOUND.

PI Tanner SM, De la Chapell A;
 WPI; 2003-441564/41.

DR N-PSDB; ADM46955.
XX
XX Characterizing acute or chronic myelogenous leukemia, or prostate cancer
PT in a patient comprises assaying for the overexpression of one or more
PT BAMLc transcripts in cells obtained from the patient.
XX
XX Disclousure; SEQ ID NO 21; 78pp; English.
XX
XX The invention relates to a method of characterizing acute myelogenous
CC leukemia (AML) in a patient by assaying for the overexpression of one or
CC more BAMLc transcripts in cells obtained from the patient, where an
CC overexpression indicates that the patient has an aggressive form of AML.
CC The methods, kits and probes are useful for characterizing acute or
CC chronic myelogenous leukemia, or prostate cancer. They are also useful
CC for detecting BAMLc overexpression. This sequence corresponds to a BAMLc
CC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
CC spliced RNA consisting of exons 1, 6 and 8.
XX
XX
SQ Sequence 149 AA;
Query Match 61.7%; Score 473.5; DB 7; Length 149;
Best Local Similarity 66.0%; Pred. No. 1.2e-43;
Matches 95; Conservative 2; Mismatches 12; Indels 35; Gaps 1;
QY 1 MGCGSRADALEPRYRESWTRETESTWLTYYDSALPSAATDSPEAGGLHA----- 53
DB 1 MGCGSRADALEPRYRESWTRETESTWLTYYDSALPSAATDSPEAGGLHSVLEAKS 60
QY 54 -----GVLEDDGPSNGVLRPAAPGGIAPPEKKNMCGT 85
DB 61 KIKAPTVDSVDEGLPSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGAIPEKKNCT 120
QY 86 QCPNSQSLSGGLPTOKONGLMWTE 109
DB 121 QCPNPQSLSSGGLPTOKONGLQCTTE 144
RESULT 11
AD081902
ID AD081902 standard; protein; 92 AA.
XX
XX AD081902;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Human dihydrogenase 10.12.
DE
XX
XX Human; enzyme; dihydrogenase 10.12; malignant tumour; inflammation;
KW immunological disease; haemopathy; HIV infection.
XX
XX Homo sapiens.
OS
XX
XX CN1344798-A.
PN
XX
XX 17-APR-2002.
PD
XX
XX 29-SEP-2000; 2000CN-00125495.
PF
XX
XX 29-SEP-2000; 2000CN-00125495.
PR
XX
XX (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
QA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-509506/55.
DR
XX
XX N-PSDB; AD081901.
XX
XX New polypeptide human dihydrogenase 10.12 and polynucleotides encoding this
PT polypeptide, useful for treating various diseases, such as malignant
PT tumour, inflammations, immunological diseases, hemopathy and HIV
PT infection.
XX
XX Claim 1; SEQ ID NO 2; 33pp; Chinese.

XX
XX The present invention discloses a new kind of polypeptide, human
CC dihydrogenase 10.12, polynucleotides encoding this polypeptide, a DNA
CC recombination process to produce the polypeptide and antagonist against
CC the polypeptide. The present invention also discloses the method of
CC applying the polypeptide in treating various diseases, such as malignant
CC tumour, inflammations, immunological diseases, hemopathy and HIV
CC infection. The present sequence is the human dihydrogenase 10.12.
XX
XX
SQ Sequence 92 AA;
Query Match 43.7%; Score 335.5; DB 5; Length 92;
Best Local Similarity 72.7%; Pred. No. 1.1e-28;
Matches 64; Conservative 9; Mismatches 10; Indels 5; Gaps 1;
QY 58 DGPSNGVLRPAAPGGIAPPEKKNMCGTQCPNSQSLSGGLPTOKONGLMWTEAKRDARM 117
DB 10 DGPEYGN-----AGCGIPNPEKKNCTQCPNPQSLSSGGLPTOKONGLQCTTEAKRDARM 64
QY 118 SARFVAISVTENIRQMDRSKRVYTCIN 145
DB 65 PAKETVITWVDSIQMDRSRRITNCVN 92
RESULT 12
AD048481
ID AD048481 standard; protein; 54 AA.
XX
XX AD048481;
AC
XX
XX 12-AUG-2004 (first entry)
DT
XX
XX Mouse PTH responsive gene protein exon 2 splice variant.
DE
XX
XX PTH responsive gene; PARG; bone-forming; bone; bone density modulation;
KW transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;
KW murine.
XX
XX Mus sp.
OS
XX
XX WO2004044152-A2.
PN
XX
XX 27-MAY-2004.
PD
XX
XX 10-NOV-2003; 2003WO-US035655.
PF
XX
XX 12-NOV-2002; 2002US-0425532P.
PR
XX
XX (AMHP) WYETH.
QA
XX
XX Robinson JA, Stojanovic-Susulic V, Babić P, Murrills RJ;
PI
XX
XX WPI; 2004-420299/39.
DR
XX
XX N-PSDB; AD048480.
XX
XX New nucleic acid fragment encoding a PARG polypeptide, useful in
PT preparing a composition for diagnosing, treating or preventing bone
PT related disorders, e.g., osteoporosis.
XX
XX Claim 9; SEQ ID NO 10; 169pp; English.
XX
XX The invention relates to a novel PTH responsive gene (PARG) fragment
CC encoding a polypeptide. The invention further comprises: a chimeric
CC construct comprising the isolated nucleic acid fragment operatively
CC linked to suitable regulatory sequences; a host cell transformed with the
CC chimeric construct; a vector comprising the nucleic acid fragment,
CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
CC obtaining a polypeptide; detecting the presence of the nucleic acid
CC fragment; an antibody that specifically binds to one or more epitopes of
CC a PARG polypeptide; a composition for regulating bone-forming activity
CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody
CC ; an agent that alters the expression of PARG gene or polypeptide;
CC determining whether an agent alters the expression of PARG mRNA;

screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DNA, an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.

Sequence 54 AA;

Query Match 38.3%; Score 294; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGCGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDGGPEAGLHAG 54
1 MGCGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDGGPEAGLHAG 54

RESULT 13
ADM46962
ID ADM46962 standard; protein; 73 AA.
XX
XX ADM46962;
XX
XX 03-JUN-2004 (first entry)
XX
XX Brain and Acute Leukemia, Cytoplasmic alternate protein #4.
XX
XX acute myelogenous leukemia; gene expression; BAALC;
XX chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
XX Cytoplasmic; exon.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 41 /note= "encoded by GCS"
XX
XX WO2003040347-A2.
XX
XX 15-MAY-2003.
XX
XX 12-NOV-2002; 2002MO-US036375.
XX
XX 09-NOV-2001; 2001US-0348210P.
XX
XX (OHIS) UNIV OHIO STATE RES FOUND.
XX
XX
XX Tanner SM, De La Chapell A;
XX
XX WPI; 2003-441564/41.
XX
XX N-PSDB; ADM46954.
XX
XX Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.

XX
XX Disclosure; SEQ ID NO 20; 78pp; English.
XX
XX The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML.
XX The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
XX
XX Sequence 73 AA;
XX
XX Query Match 37.5%; Score 288; DB 7; Length 73;
XX Best Local Similarity 91.4%; Pred. No. 1.3e-23;
XX Matches 53; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 MGCGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDGGPEAGLHAG 58
1 MGCGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDGGPEAGLHAG 58

RESULT 14
ADM46960
ID ADM46960 standard; protein; 54 AA.
XX
XX ADM46960;
XX
XX 03-JUN-2004 (first entry)
XX
XX Brain and Acute Leukemia, Cytoplasmic alternate protein #2.
XX
XX acute myelogenous leukemia; gene expression; BAALC;
XX chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
XX Cytoplasmic; exon.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 41 /note= "encoded by GCS"
XX
XX WO2003040347-A2.
XX
XX 15-MAY-2003.
XX
XX 12-NOV-2002; 2002MO-US036375.
XX
XX 09-NOV-2001; 2001US-0348210P.
XX
XX (OHIS) UNIV OHIO STATE RES FOUND.
XX
XX
XX Tanner SM, De La Chapell A;
XX
XX WPI; 2003-441564/41.
XX
XX N-PSDB; ADM46952.
XX
XX Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
XX
XX Disclosure; SEQ ID NO 18; 78pp; English.
XX
XX The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML.
XX The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative

CC spliced RNA consisting of exons 1, 6 and 8.
 XX Sequence 54 AA;
 SQ

Query Match 36.2%; Score 278; DB 7; Length 54;
 Best Local Similarity 94.4%; Pred. No. 1.1e-22;
 Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIEPRYYESWTRTETSTWLTYYTDSALPSAAATDSGPAGGLHAG 54
 Db 1 MCGCGSRADAIEPRYYESWTRTETSTWLTYYTDSALPSAAATDSGPAGGLHAG 54

RESULT 15
 ADO48477
 ID ADO48477 standard; protein, 54 AA.
 XX ADO48477;
 AC
 XX 12-AUG-2004 (first entry)
 DT
 XX Human PTH responsive gene protein exon 2 splice variant.
 DE
 XX PTH responsive gene; PARGB; bone-forming; bone; bone density modulation;
 KM transgenic animal; osteopathic; gene therapy; osteoporosis; human.
 XX
 OS Homo sapiens.
 XX
 XX MO2004044152-A2.
 PN
 XX 27-MAY-2004.
 PD
 XX 10-NOV-2003; 2003WO-US035655.
 PF
 XX 12-NOV-2002; 2002US-0425532P.
 PR
 XX (AMHP) WYETH.
 PA
 XX Robinson JA, Stojanovic-Svabljic V, Babić P, Murrills RJ;
 PI
 XX WPI: 2004-430299/39.
 DR N-PSDB; ADO48476.
 XX
 XX New nucleic acid fragment encoding a PARGB polypeptide, useful in
 PT preparing a composition for diagnosing, treating or preventing bone
 PT related disorders, e.g., osteoporosis.
 XX
 XX Claim 9; SEQ ID NO 6; 169pp; English.
 PS
 XX The invention relates to a novel PTH responsive gene (PARGB) fragment
 CC encoding a polypeptide. The invention further comprises: a chimeric
 CC construct comprising the isolated nucleic acid fragment operatively
 CC linked to suitable regulatory sequences; a host cell transformed with the
 CC chimeric construct; a vector comprising the nucleic acid fragment;
 CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
 CC obtaining a polypeptide; detecting the presence of the nucleic acid
 CC fragment; an antibody that specifically binds to one or more epitopes of
 CC a PARGB polypeptide; a composition for regulating bone-forming activity
 CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody
 CC ; an agent that alters the expression of PARGB gene or polypeptide;
 CC determining whether an agent alters the expression of PARGB mRNA;
 CC screening agents for effectiveness in altering expression of the nucleic
 CC acid fragment; screening for agents useful for treating bone related
 CC disorders; evaluating the efficacy of a treatment of a bone related
 CC disorder in a subject; identifying polypeptides capable of binding to
 CC PARGB; monitoring the effectiveness of treatment of a subject with a bone
 CC related agent; a transgenic animal comprising the DNA; an animal model
 CC for the study of bone density modulation comprising a first group of
 CC animals composed of the transgenic animal and a second group of control
 CC animals; studying bone mass determinants; studying the modulation of bone
 CC mass; studying an effect of PARGB on bone disorders; identifying an agent
 CC for treating bone related disorders; identifying whether an agent which
 CC has bone forming activity; and a stably transfected cell line comprising

CC two constructs, the first construct comprising a ligand binding domain
 CC linked to a DNA binding domain which is linked to an activation domain
 CC all of which expression is driven by a constitutive promoter, the second
 CC construct comprising multiple copies of DNA binding elements linked to a
 CC minimal promoter which is linked to PARGB cDNA, where upon the addition
 CC of chemical inducer, transcription of PARGB gene is induced. The PARGB
 CC polynucleotide has osteopathic activity. The PTH responsive gene may be
 CC used to treat disorders by gene therapy. The nucleic acid is useful in
 CC preparing a composition for diagnosing, treating or preventing bone
 CC related disorders, e.g., osteoporosis. This sequence represents a PTH
 CC responsive gene protein of the invention.
 XX
 XX Sequence 54 AA;
 SQ

Query Match 36.2%; Score 278; DB 8; Length 54;
 Best Local Similarity 94.4%; Pred. No. 1.1e-22;
 Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIEPRYYESWTRTETSTWLTYYTDSALPSAAATDSGPAGGLHAG 54
 Db 1 MCGCGSRADAIEPRYYESWTRTETSTWLTYYTDSALPSAAATDSGPAGGLHAG 54

Search completed: May 20, 2006, 20:18:06
 Job time : 86 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 21:10:42 ; Search time 51 Seconds

(without alignments)
248,862 Million cell updates/sec

Title: US-10-705-716a-2

Perfect score: 1 MGCGSGADALIEPRYSWT.....VTENIRMDRSKRVTKNCIN 145

Sequence: 1 MGCGSGADALIEPRYSWT.....VTENIRMDRSKRVTKNCIN 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA+
1: /EMC_Celerra_SIDS3/prodata/2/iaa/5.COMB.pcp.*
2: /EMC_Celerra_SIDS3/prodata/2/iaa/6.COMB.pcp.*
3: /EMC_Celerra_SIDS3/prodata/2/iaa/7.COMB.pcp.*
4: /EMC_Celerra_SIDS3/prodata/2/iaa/H.COMB.pcp.*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCMS.COMB.pcp.*
6: /EMC_Celerra_SIDS3/prodata/2/iaa/RE.COMB.pcp.*
7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92.5	12.1	694	2	US-09-949-016-7117 Sequence 7117, App
2	92.5	12.1	778	7	5198347-4 Patent No. 5198347
3	84	11.0	726	2	US-09-328-352-8115 Sequence 8115, App
4	83.5	10.9	700	2	US-09-408-647A-2 Sequence 2, Appl
5	83	10.8	1433	2	US-09-487-558B-60 Sequence 60, Appl
6	79.5	10.4	286	2	US-09-071-035-176 Sequence 176, App
7	79.5	10.4	286	2	US-10-206-576-176 Sequence 176, App
8	79.5	10.4	305	2	US-09-071-035-174 Sequence 174, App
9	79.5	10.4	305	2	US-10-206-576-174 Sequence 174, App
10	79.5	10.4	661	2	US-10-076-622-552 Sequence 552, App
11	79.5	10.4	661	2	US-10-124-805-552 Sequence 552, App
12	79.5	10.4	1013	2	US-10-076-622-553 Sequence 553, App
13	79.5	10.4	1013	2	US-10-124-805-553 Sequence 553, App
14	78.5	10.2	2516	2	US-08-374-077C-2 Sequence 2, Appl
15	78.5	10.2	2516	2	US-08-895-590-2 Sequence 2, Appl
16	78.5	10.2	2516	2	US-09-539-879A-2 Sequence 2, Appl
17	78	10.2	724	2	US-09-121-964-1 Sequence 1, Appl
18	78	10.2	885	2	US-09-914-259-10 Sequence 10, Appl
19	77.5	10.1	215	2	US-09-220-528-104 Sequence 104, App
20	77.5	10.1	445	2	US-09-620-405B-473 Sequence 473, App
21	77.5	10.1	445	2	US-09-433-826B-473 Sequence 473, App
22	77.5	10.1	445	2	US-09-604-287A-473 Sequence 473, App
23	77.5	10.1	445	2	US-09-834-759-473 Sequence 473, App
24	77.5	10.1	445	2	US-09-590-751A-473 Sequence 473, App
25	77.5	10.1	445	2	US-09-581-621-473 Sequence 473, App
26	77.5	10.1	445	2	US-09-551-621A-473 Sequence 473, App

27	77.5	10.1	445	2	US-10-076-622-473 Sequence 473, App
28	77.5	10.1	445	2	US-10-124-805-473 Sequence 473, App
29	76.5	10.0	316	2	US-09-248-796A-16753 Sequence 16753, A
30	74.5	9.7	198	2	US-09-252-991A-23204 Sequence 23204, A
31	74.5	9.7	650	2	US-09-620-405B-469 Sequence 469, App
32	74.5	9.7	650	2	US-09-433-826B-469 Sequence 469, App
33	74.5	9.7	650	2	US-09-604-287A-469 Sequence 469, App
34	74.5	9.7	650	2	US-09-834-759-469 Sequence 469, App
35	74.5	9.7	650	2	US-09-590-751A-469 Sequence 469, App
36	74.5	9.7	650	2	US-09-551-621-469 Sequence 469, App
37	74.5	9.7	650	2	US-10-076-622-469 Sequence 469, App
38	74.5	9.7	650	2	US-10-124-805-469 Sequence 469, App
39	74.5	9.7	743	2	US-09-620-405B-494 Sequence 494, App
40	74.5	9.7	743	2	US-09-834-759-494 Sequence 494, App
41	74.5	9.7	743	2	US-10-076-622-494 Sequence 494, App
42	74.5	9.7	743	2	US-10-124-805-494 Sequence 494, App
43	74.5	9.7	1002	2	US-09-620-405B-475 Sequence 475, App
44	74.5	9.7	1002	2	US-09-604-287A-475 Sequence 475, App
45	74.5	9.7	1002	2	US-09-604-287A-475 Sequence 475, App

ALIGNMENTS

```
RESULT 1
US-09-949-016-7117
Sequence 7117, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7117
LENGTH: 694
TYPE: PRT
ORGANISM: Human
US-09-949-016-7117
Query Match 12.1%; Score 92.5; DB 2; Length 694;
Best local similarity 31.9%; Pred. No. 0.12;
Matches 30; Conservative 7; Mismatches 32; Indels 25; Gaps 3;
QY 31 TDSALPSAATDGEAGGLH-----AGVLEDGSSNGVLRPAAP-- 71
DB 233 TDSRQSPAKNSKRVSHNQHPQSPAVPTYPGPPAPASALSTPGRNNGVAPAPAPS 292
QY 72 --GIANPEKQNCCTGCNCSGLS-----SGPRT 99
DB 293 ALGPKASPAHSHSGTPAPYAOAVAPAPSPGPT 326
RESULT 2
5198347-4
Patent No. 5198347
APPLICANT: MILLER, LOUIS H.; ADAMS, JOHN H.; KASLOW,
DAVIC C.; FANG, XIANGDOUG
TITLE OF INVENTION: DNA ENCODING PLASMIDIUM VIVAX AND
PLASMIDIUM KNOWLEST DUPLY RECEPTOR
NUMBER OF SEQUENCES: 27
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,837
FILING DATE: 20-JUL-1990
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SEQ ID NO.4:
LENGTH: 778
5198347-4

Query Match 12.1%; Score 92.5; DB 7; Length 778;
Best Local Similarity 33.0%; Pred. No. 0.14;
Matches 29; Conservative 12; Mismatches 44; Indels 3; Gaps 3;

QY 31 TDSALPSAATDSGPEAGLHAGVLEDPSSNGV-LRPAAPGIANPEKMC-GTQCP 88
DB 352 TVSDVDPVGGKDGSTGASHALAGEVHNGTDTPEKDEKADPOKDIYVKGQDT 411

QY 89 NSQSLSS-GPLTKONGLMTTEAKRDAK 115
DB 412 DDRSGSLGPHPTDERATLGETHMKDTE 439

RESULT 3

US-09-328-352-8115
Sequence 8115, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8115
LENGTH: 726

TYPE: PRT
ORGANISM: Acinetobacter baumannii

US-09-328-352-8115

Query Match 11.0%; Score 84; DB 2; Length 726;
Best Local Similarity 35.1%; Pred. No. 1.2;
Matches 27; Conservative 8; Mismatches 22; Indels 20; Gaps 4;

QY 2 GCGGSRDAIPRYESWTRETESWTLYTSDALPSA--ATDSG-----PEAGLHAG 54
DB 181 GFGAGREVWPDVDVNGDEKE--WLAHRSEALAGSNLAATENGILYVNP----- 231

QY 55 VLEDGSSNGVLRPAAP 71
DB 232 ----GPGASGDPKSAAP 244

RESULT 4

US-09-408-647A-2
Sequence 2, Application US/09408647A
Patent No. 6399858

GENERAL INFORMATION:

APPLICANT: Kobayashi, Donald
TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas

FILE REFERENCE: Rut-Cook 98-0090
CURRENT APPLICATION NUMBER: US/09/408,647A
CURRENT FILING DATE: 1999-08-26

PRIOR APPLICATION NUMBER: 60/098,036
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2

LENGTH: 700
TYPE: PRT
ORGANISM: Stenotrophomonas maltophilia

FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1) ... (41)

NAME/KEY: DOMAIN
LOCATION: (196) ... (290)
NAME/KEY: DOMAIN

LOCATION: (330) ... (483)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank No. 6399858 AF014950
DATABASE ENTRY DATE: 1997-09-23
US-09-408-647A-2

Query Match 10.9%; Score 83.5; DB 2; Length 700;
Best Local Similarity 24.0%; Pred. No. 1.4;
Matches 31; Conservative 14; Mismatches 57; Indels 27; Gaps 2;

QY 26 TWLYTSDALPSAATDSGPEAGLHAGVLEDPSSNGVLRPAAPGIANPEKMC----- 81
DB 159 TWANASGSHTFKAVATDNNNAVTSSATVSVTYASNDTTPSPVPGGLSPSKATTVN 218

QY 82 -----NCG-----TQCPNSQSLSSGPLTKONGLMTTEAKRDAKMS 118
DB 219 LVMSAATDNGSGGVAGYDYVRNGSLVSPSATQYTDGGLTASTAYTYTARADNAGNAS 278

QY 119 AREVAISVT 127
DB 279 AQSGSISVT 287

RESULT 5

US-09-487-558B-60
Sequence 60, Application US/09487558B
Patent No. 6943356

GENERAL INFORMATION:

APPLICANT: Busby, Robert
APPLICANT: Cali, Brian

APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug

APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary

APPLICANT: Milne, Todd
APPLICANT: Royer, John

APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir

APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric

TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.130

CURRENT APPLICATION NUMBER: US/09/487,558B
CURRENT FILING DATE: 2000-01-19

PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0

SEQ ID NO 60
LENGTH: 1433

TYPE: PRT
ORGANISM: Saccharomyces cerevisiae

US-09-487-558B-60

Query Match 10.8%; Score 83; DB 2; Length 1433;
Best Local Similarity 29.4%; Pred. No. 4.4;
Matches 33; Conservative 15; Mismatches 50; Indels 12; Gaps 4;

QY 36 LPSAATDSGPEAGLHAGVLEDPSSNGVLRPAAPGIANPEKMCCTGCPNSQSIS 95
DB 927 LPPATTTSLKPLVSGSGKSLNKRQTPVYK-----ENPEHEIYLGNDNNNNSEA 979

QY 96 G--PLTKONGLMTTEAKRDAKMSAREVAISVTENIR--QMDRSKRV 140
DB 980 GHSPTWTNTGNKRLKYEKDAKR-NAKDGISKGENAHNFQNDYKKNMS 1027

RESULT 6

US-09-071-035-176
Sequence 176, Application US/09071035
Patent No. 6448043

GENERAL INFORMATION:

```

1  APPLICANT: GIL H. Choi
2  TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
3  NUMBER OF SEQUENCES: 496
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Human Genome Sciences, Inc.
6  STREET: 9410 Key West Avenue
7  CITY: Rockville
8  STATE: Maryland
9  COUNTRY: USA
10 ZIP: 20850
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
14 COMPUTER: HP Vectra 486/33
15 OPERATING SYSTEM: MSDOS version 6.2
16 SOFTWARE: ASCII text
17
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/071,035
20 FILING DATE:
21 CLASSIFICATION:
22
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER:
25 FILING DATE:
26
27 ATTORNEY/AGENT INFORMATION:
28 NAME: A. Anders Brookes
29 REGISTRATION NUMBER: 36,373
30 REFERENCE/DOCKET NUMBER: PB369P2
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (301) 309-8504
33 TELEFAX: (301) 309-8512
34
35 INFORMATION FOR SEQ ID NO: 176:
36
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 286 amino acids
39 TYPE: amino acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42
43 MOLECULE TYPE: protein
44
45 OS-09-071-035-176

```

```

RESULT 7
US-10-206-576-176
; Sequence 176, Application US/10206576
; Patent No. 6913907
;
; GENERAL INFORMATION:
;
; APPLICANT: Choi et al.
;
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;
; NUMBER OF SEQUENCES: 497
;
; CORRESPONDENCE ADDRESSES:
;
; ADDRESSEE: Human Genome Sciences, Inc.
;
; STREET: 9410 Key West Avenue
;
; CITY: Rockville
;
; STATE: Maryland
;
; COUNTRY: USA
;
; ZIP: 20850
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: CD-R
;
; COMPUTER: Dell Latitude

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1      OPERATING SYSTEM: Windows 98
2      SOFTWARE: ASCII Text
3
4      CURRENT APPLICATION DATA:
5      APPLICATION NUMBER: US/10/206,576
6      FILING DATE: 29-Jul-2002
7      CLASSIFICATION: <Unknown>
8
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: US 09/071,035
11     FILING DATE: 1998-05-04
12     APPLICATION NUMBER: US 60/046,655
13     FILING DATE: 1997-05-16
14     APPLICATION NUMBER: US 60/044,031
15     FILING DATE: 1997-05-06
16     APPLICATION NUMBER: US 60/066,009
17     FILING DATE: 1997-11-14
18
19     ATTORNEY/AGENT INFORMATION:
20     NAME: Hyman, Mark J.
21     REGISTRATION NUMBER: 46,789
22     REFERENCE/DOCKET NUMBER: PB369PID1D
23
24     INFORMATION FOR SEQ ID NO: 176:
25     SEQUENCE CHARACTERISTICS:
26     LENGTH: 286 amino acids
27     TYPE: amino acid
28     STRANDEDNESS: single
29     TOPOLOGY: linear
30
31     MOLECULE TYPE: protein
32
33     SEQUENCE DESCRIPTION: SEQ ID NO: 176:
34
35     US-10-206-576-176

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Query Match 10.4%; Score 79.5; DB 2; Length 286;
Best Local Similarity 26.6%; Pred. No. 1.1;
Matches 47; Conservative 16; Mismatches 73; Indels 4; Gaps 9;

QY 3 CGG-----SRDAIEPRYYESW---TRETSTWLTYYTSDALPSAAAT-DSGPENG 49
Db 1 CGGGKSTENTWDSRSSAAESTTVESTYASATKESSSK-ATTKSSDAPKPSGTTADSKATAS 59
QY 50 GLHAGVLEDPGSSNGVLRPAAPGCIANPEKKN-CCTGCPN---SGSLSSGPIITGKONAL 105
Db 60 STGEA-----ANNGSAEKQSPAKKANPDDQANQVLANPFGQGLPQAILTSTNNF 113
QY 106 WTTAARDAKRMASAREVAISVTENIRQMD-RSKRYVT-----KNCIN 145
Db 114 LTAATTQADQNNFVLYYAEKEKALPVDARVNUQLTPISSFEKTYGSDAEAKNAVN 170

RESULT 8
US-09-071-035-174
; Sequence 174, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

```


APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.

MOLECULE TYPE: protein
US-08-374-077C-2

Query Match 10.2%; Score 78.5; DB 2; length 2516;
 Best Local Similarity 22.4%; Pred. No. 33;
 Matches 39; Conservative 21; Mismatches 61; Indels 53; Gaps 8;
 QY 3 CCGSRADAIERY--YESWTEFTESTWLTYYDSALPSAATDGPAGGHAAGVLEDGP 60
 DB 207 CCGGGGISAAPPRLTPPEBAMQLOPQ-----NSVTSAGTSSFSFGG-----GR 249
 QY 61 SSNGVLPAAPGIANPEKKNK-----GTQC-----PNS 90
 DB 250 DDNSY--SAVGGSSSSNSCNCITGDNSTLHGLGVGDVCSFLADCDNSDDDDGDPNN 307
 QY 91 QSLSSGPL-TOKONGMTTEAKRDARMSAREVAISVTENIRQMRKRVTKNC 143
 DB 308 QDLSSQTLRTAIVAAVAAAKQAQESGLADCE-SFSDRRQDADEPVRITQDC 360

QY 91 QSLSSGPL-TOKONGMTTEAKRDARMSAREVAISVTENIRQMRKRVTKNC 143
 DB 308 QDLSSQTLRTAIVAAVAAAKQAQESGLADCE-SFSDRRQDADEPVRITQDC 360
 Search completed: May 20, 2006, 21:21:21
 Job time : 52 secs

RESULT 15
 US-08-895-590-2
 ; Sequence 2, Application US/08895590
 ; Patent No. 6207410
 ; GENERAL INFORMATION:
 ; APPLICANT: Hall, Linda M.
 ; APPLICANT: Ren, Dejian
 ; APPLICANT: Zheng, Wei
 ; APPLICANT: Dubald, Manuel Marcel Paul
 ; TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314-3187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/895,590
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/374,888
 ; FILING DATE: 19-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McGowan, Malcolm M.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 022650-263
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2516 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-895-590-2

Query Match 10.2%; Score 78.5; DB 2; length 2516;
 Best Local Similarity 22.4%; Pred. No. 33;
 Matches 39; Conservative 21; Mismatches 61; Indels 53; Gaps 8;

QY 3 CCGSRADAIERY--YESWTEFTESTWLTYYDSALPSAATDGPAGGHAAGVLEDGP 60
 DB 207 CCGGGGISAAPPRLTPPEBAMQLOPQ-----NSVTSAGTSSFSFGG-----GR 249
 QY 61 SSNGVLPAAPGIANPEKKNK-----GTQC-----PNS 90
 DB 250 DDNSY--SAVGGSSSSNSCNCITGDNSTLHGLGVGDVCSFLADCDNSDDDDGDPNN 307

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OM protein - protein search, using sw model

Run on: May 20, 2006, 21:21:43 ; Search time 74 Seconds
(without alignments)
907.651 Million cell updates/sec

Title: US-10-705-716A-2

Perfect score: 767
Sequence: 1 MCGGSRADAIIPRYESWT.....VTENIRQMDRSKRYTKNCIN 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/prodata/2/pubppa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/pubppa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	767	100.0	145	4	US-10-705-716A-2
2	746	97.3	145	4	US-10-705-716A-8
3	645	84.1	145	4	US-10-293-239-17
4	645	84.1	145	4	US-10-177-390-30
5	645	84.1	145	4	US-10-705-716A-4
6	617.5	80.5	180	4	US-10-293-239-19
7	473.5	61.7	149	4	US-10-293-239-21
8	294	38.3	54	4	US-10-705-716A-10
9	288	37.5	73	4	US-10-293-239-20
10	278	36.2	54	4	US-10-293-239-18
11	272	35.5	80	4	US-10-705-716A-6
12	272	35.5	80	4	US-10-293-239-32
13	140	18.3	25	4	US-10-293-239-37
14	99	12.9	18	4	US-10-293-239-35
15	94	12.3	147	4	US-10-767-701-48905
16	93	12.1	394	4	US-10-425-115-236244
17	89	11.6	16	4	US-10-705-716A-11
18	87.5	11.4	260	5	US-10-450-763-40258
19	87.5	11.4	592	5	US-10-450-763-45966
20	85.5	11.1	264	4	US-10-425-115-275422
21	85.5	11.1	274	4	US-10-425-114-65588
22	85	11.0	450	4	US-10-437-963-137075
23	84	11.0	718	4	US-10-282-122A-45268
24	83	10.8	1433	3	US-09-801-368-60
25	83	10.8	1433	3	US-10-149-310-112
26	82.5	10.8	514	6	US-11-188-298-18211
27	82.5	10.8	539	4	US-10-424-599-227399

28	82.5	10.8	609	4	US-10-437-963-144983	Sequence 144983,
29	82	10.7	339	5	US-10-494-495-9	Sequence 9, Appl1
30	82	10.7	1491	4	US-10-437-963-140197	Sequence 140197,
31	82	10.7	1597	4	US-10-437-963-180225	Sequence 180225,
32	81.5	10.6	600	4	US-10-408-765A-1945	Sequence 1945, Ap
33	81.5	10.6	950	5	US-10-745-237-254	Sequence 254, App
34	81	10.6	670	4	US-10-156-761-14107	Sequence 14107, A
35	80.5	10.5	275	5	US-10-450-763-45790	Sequence 45790, A
36	80.5	10.5	275	5	US-10-450-763-51738	Sequence 51738, A
37	80.5	10.5	350	4	US-10-425-114-43318	Sequence 43318, A
38	80.5	10.5	508	4	US-10-437-963-188141	Sequence 188141,
39	79.5	10.4	286	3	US-09-071-035-176	Sequence 176, App
40	79.5	10.4	286	4	US-10-206-576-176	Sequence 176, App
41	79.5	10.4	286	5	US-10-912-362-174	Sequence 174, App
42	79.5	10.4	305	3	US-09-071-035-174	Sequence 174, App
43	79.5	10.4	305	4	US-10-206-576-174	Sequence 174, App
44	79.5	10.4	305	5	US-10-912-362-174	Sequence 174, App
45	79.5	10.4	661	4	US-10-007-805-552	Sequence 552, App

ALIGNMENTS

```

RESULT 1
US-10-705-716A-2
; Sequence 2, Application US/10705716A
; Publication No. US20040146906A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Suenilic, Vedrana
; APPLICANT: Bablj, Philip
; TITLE OF INVENTION: A Novel PTH Responsive Gene
; FILE REFERENCE: AM100401
; CURRENT APPLICATION NUMBER: US/10/705, 716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425, 532
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Rat
US-10-705-716A-2

Query Match      100.0%; Score 767; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.4e-69;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MCGGSRADAIIPRYESWTRETSTWLTYSDDALPSAAATDSCGEAGIHAQVLEDPG 60
DB      1 MCGGSRADAIIPRYESWTRETSTWLTYSDDALPSAAATDSCGEAGIHAQVLEDPG 60
QY      61 SNGVLRPAAPGIANPEKKNCGTQCPNSQSISGFLTKOKNGLWTTBAKDDAKMSAR 120
DB      61 SNGVLRPAAPGIANPEKKNCGTQCPNSQSISGFLTKOKNGLWTTBAKDDAKMSAR 120
QY      121 EVAISTENIRQMDRSKRYTKNCIN 145
DB      121 EVAISTENIRQMDRSKRYTKNCIN 145
QY      121 EVAISTENIRQMDRSKRYTKNCIN 145
DB      121 EVAISTENIRQMDRSKRYTKNCIN 145

RESULT 2
US-10-705-716A-8
; Sequence 8, Application US/10705716A
; Publication No. US20040146906A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Suenilic, Vedrana
; APPLICANT: Bablj, Philip
; APPLICANT: Murrills, Richard John
; TITLE OF INVENTION: A Novel PTH Responsive Gene

```


FILE REFERENCE: AM100401
CURRENT APPLICATION NUMBER: US/10/705, 716A
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: US 60/425,532
PRIOR FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 145
TYPE: PRT
ORGANISM: Mouse
US-10-705-716A-8

Query Match 97.3%; Score 746; DB 4; Length 145;
Best Local Similarity 97.2%; Pred. No. 7.1e-67;
Matches 141; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDGP 60
DB 1 MCGGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDGL 60
QY 61 SSSGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
DB 61 SSSGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 3
US-10-293-239-17
Sequence 17, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
APPLICANT: Tanner, Stephan
TITLE OF INVENTION: BALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-239-17

Query Match 84.1%; Score 645; DB 4; Length 145;
Best Local Similarity 83.4%; Pred. No. 1e-56;
Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDGP 60
DB 1 MCGGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDGL 60
QY 61 SSSGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
DB 61 PSNGVPRSTAPGIPPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMPAK 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 4
US-10-177-390-30
Sequence 30, Application US/10177390
Publication No. US20030143743A1
GENERAL INFORMATION:

APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerp Innovatiecentrum
TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-390-30

Query Match 84.1%; Score 645; DB 4; Length 145;
Best Local Similarity 83.4%; Pred. No. 1e-56;
Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDGP 60
DB 1 MCGGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDGL 60
QY 61 SSSGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
DB 61 PSNGVPRSTAPGIPPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMPAK 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 5
US-10-705-716A-4
Sequence 4, Application US/10705716A
Publication No. US20040146906A1
GENERAL INFORMATION:
APPLICANT: Robinson, John Allen
APPLICANT: Stojanovic-Susulic, Vedrana
APPLICANT: Bablj, Philip
APPLICANT: Murrille, Richard John
TITLE OF INVENTION: A Novel PTH Responsive Gene
FILE REFERENCE: AM100401
CURRENT APPLICATION NUMBER: US/10/705,716A
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: US 60/425,532
PRIOR FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-10-705-716A-4

Query Match 84.1%; Score 645; DB 4; Length 145;
Best Local Similarity 83.4%; Pred. No. 1e-56;
Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDGP 60
DB 1 MCGGSRADAIERPRYESWTRTESTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDGL 60
QY 61 SSSGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
DB 61 PSNGVPRSTAPGIPPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMPAK 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 6

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us-10-293-239-19
; Sequence 19, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-19
```

```
Query Match      80.5%; Score 617.5; DB 4; Length 180;
Best Local Similarity 67.2%; Pred. No. 8.1e-54;
Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;
```

```
QY 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGLHA----- 53
DB 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDAPSAAPDGPAGGLHSLAEKES 60
QY 54 -----GVLEDPSSNGVLRPAAPGSIAPKKNKCGT 85
DB 61 KIRAPDVSDEGLFSASKMAPLAVFSHGMLEDLPNSGVFRSTAPGIPPEKTKNCET 120
QY 86 QCPNSQSLSSGPILOKONGIMTTEAKDKAKMSAREVAISVENIRQWDSKRYTKNCIN 145
DB 121 QCPNPQSLSSGPILOKONGIQTTEAKDKAKMPAKETVINTVDSIQWDSRRTTKNCVN 180
```

RESULT 7

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US-10-293-239-21
; Sequence 21, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-21
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Query Match      61.7%; Score 473.5; DB 4; Length 149;
Best Local Similarity 66.0%; Pred. No. 2e-39;
Matches 95; Conservative 2; Mismatches 12; Indels 35; Gaps 1;
QY 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGLHA----- 53
DB 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDAPSAAPDGPAGGLHSLAEKES 60
QY 54 -----GVLEDPSSNGVLRPAAPGSIAPKKNKCGT 85
DB 61 KIRAPDVSDEGLFSASKMAPLAVFSHGMLEDLPNSGVFRSTAPGIPPEKTKNCET 120
QY 86 QCPNSQSLSSGPILOKONGIMTTE 109
DB 121 QCPNPQSLSSGPILOKONGIQTTE 144
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RESULT 8
US-10-705-716A-10
; Sequence 10, Application US/10705716A
; Publication No. US20040146906A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Susulic, Vedrana
; APPLICANT: Babilj, Philip
; APPLICANT: Murrills, Richard John
; TITLE OF INVENTION: A Novel PTH Responsive Gene
; FILE REFERENCE: AM100401
; CURRENT APPLICATION NUMBER: US/10/705,716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425,532
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Mouse
US-10-705-716A-10
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```
Query Match      38.3%; Score 294; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 6.6e-22;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGLHAG 54
DB 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGLHAG 54
```

RESULT 9

```
US-10-293-239-20
; Sequence 20, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-20
```

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Query Match      37.5%; Score 288; DB 4; Length 73;
Best Local Similarity 91.4%; Pred. No. 3.9e-21;
Matches 53; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGLHAGVLEED 58
DB 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDAPSAAPDGPAGGLHSLAEKES 58
RESULT 10
US-10-293-239-18
; Sequence 18, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
```

;; CURRENT APPLICATION NUMBER: US/10/293,239
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: US 60/348,210
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 18
;; LENGTH: 54
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-239-18

Query Match 36.2%; Score 278; DB 4; Length 54;
Best Local Similarity 94.4%; Pred. No. 2,7e-20;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIERPRYSWTRETESTWLTYYTDSALPSAAATDSCGPEAGGILHAG 54
Db 1 MCGGSRADAIERPRYSWTRETESTWLTYYTDSALPSAAAPDSGPEAGGILHSG 54

RESULT 11
US-10-705-716a-6
;; Sequence 6, Application US/10705716A
;; Publication No. US20040146906A1
;; GENERAL INFORMATION:
;; APPLICANT: Robinson, John Allen
;; APPLICANT: Stojanovic-Svuljic, Vedrana
;; APPLICANT: Babil, Philip
;; APPLICANT: Murrills, Richard John
;; TITLE OF INVENTION: A Novel PTH Responsive Gene
;; FILE REFERENCE: AM100401
;; CURRENT APPLICATION NUMBER: US/10/705,716A
;; CURRENT FILING DATE: 2003-11-10
;; PRIOR APPLICATION NUMBER: US 60/425,532
;; PRIOR FILING DATE: 2002-11-12
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 6
;; LENGTH: 54
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-705-716a-6

Query Match 36.2%; Score 278; DB 4; Length 54;
Best Local Similarity 94.4%; Pred. No. 2,7e-20;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIERPRYSWTRETESTWLTYYTDSALPSAAATDSCGPEAGGILHAG 54
Db 1 MCGGSRADAIERPRYSWTRETESTWLTYYTDSALPSAAAPDSGPEAGGILHSG 54

RESULT 12
US-10-293-239-22
;; Sequence 22, Application US/10293239
;; Publication No. US20030119043A1
;; GENERAL INFORMATION:
;; APPLICANT: Tanner, Stephen
;; APPLICANT: de la Chapelle, Albert
;; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
;; FILE REFERENCE: 22727/04101
;; CURRENT APPLICATION NUMBER: US/10/293,239
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: US 60/348,210
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 22
;; LENGTH: 80
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-239-22

Query Match 35.5%; Score 272; DB 4; Length 80;
Best Local Similarity 94.3%; Pred. No. 1,8e-19;
Matches 50; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIERPRYSWTRETESTWLTYYTDSALPSAAATDSCGPEAGGILHAG 53
Db 1 MCGGSRADAIERPRYSWTRETESTWLTYYTDSALPSAAAPDSGPEAGGILHSG 53

RESULT 13
US-10-293-239-37
;; Sequence 37, Application US/10293239
;; Publication No. US20030119043A1
;; GENERAL INFORMATION:
;; APPLICANT: Tanner, Stephen
;; APPLICANT: de la Chapelle, Albert
;; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
;; FILE REFERENCE: 22727/04101
;; CURRENT APPLICATION NUMBER: US/10/293,239
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: US 60/348,210
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 37
;; LENGTH: 25
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-239-37

Query Match 18.3%; Score 140; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RADAIERPRYSWTRETESTWLTYYT 31
Db 1 RADAIERPRYSWTRETESTWLTYYT 25

RESULT 14
US-10-293-239-35
;; Sequence 35, Application US/10293239
;; Publication No. US20030119043A1
;; GENERAL INFORMATION:
;; APPLICANT: Tanner, Stephen
;; APPLICANT: de la Chapelle, Albert
;; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
;; FILE REFERENCE: 22727/04101
;; CURRENT APPLICATION NUMBER: US/10/293,239
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: US 60/348,210
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 35
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-239-35

Query Match 12.9%; Score 99; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DATEPRYSWTRETEST 26
Db 1 DATEPRYSWTRETEST 18

RESULT 15
US-10-767-701-48905
;; Sequence 48905, Application US/10767701

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; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 48905
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3476-020-P1-K1-A12.pep
US-10-767-701-48905

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Query Match      12.3%; Score 94; DB 4; Length 147;
Best Local Similarity 27.5%; Pred. No. 0.32;
Matches 30; Conservative 17; Mismatches 52; Indels 10; Gaps 3;

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QY 36 LPSAAATDSGPEAGLHAGVLEDPSSNGVLRPAAPGIANPEKKNCTGCPNSQS--- 92
Db 29 LPAALAPEDAGAEAGADNGAHGPHRG---QAEAGAGARDGALHCGPPCPHSDSCIG 84
QY 93 --LSSGPLETKO-NGLWTEAKRDAKMSAREVAISVTENIRQMDRSKR 138
Db 85 RMTSTGTSGHRPCSGGLSVQLLRQMPRSSAEQVRKEIKQIQEORRYR 133

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Search completed: May 20, 2006, 21:23:19
Job time : 75 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2006, 21:23:34 ; Search time 5 Seconds
(without alignments)
61.947 Million cell updates/sec

Title: US-10-705-716a-2

Perfect score: 767
Sequence: 1 MCGGSGRAAIEPRYBSWT.....VTENINQMRSKVTYKNCIN 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.New.*
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2: /BMC_Celerra_SIDS3/prodata/2/pubpaa/US06_NEW_PUB_Pep.*
3: /BMC_Celerra_SIDS3/prodata/2/pubpaa/US07_NEW_PUB_Pep.*
4: /BMC_Celerra_SIDS3/prodata/2/pubpaa/US08_NEW_PUB_Pep.*
5: /BMC_Celerra_SIDS3/prodata/2/pubpaa/PCT_NEW_PUB_Pep.*
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7: /BMC_Celerra_SIDS3/prodata/2/pubpaa/US10_NEW_PUB_Pep.*
8: /BMC_Celerra_SIDS3/prodata/2/pubpaa/US60_NEW_PUB_Pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64.5	8.4	356	US-10-505-928-391	Sequence 391, App
2	64.5	8.4	413	US-10-511-937-2428	Sequence 2428, App
3	64	8.3	262	US-10-370-959-131	Sequence 131, App
4	64	8.3	474	US-11-301-554-1812	Sequence 1812, App
5	63.5	8.3	443	US-10-511-937-2464	Sequence 2464, App
6	62	8.1	2671	US-10-505-928-784	Sequence 784, App
7	61.5	8.0	404	US-11-251-465-23	Sequence 23, App
8	61.5	8.0	1075	US-10-322-936-48	Sequence 48, App
9	60.5	7.9	353	US-10-505-928-851	Sequence 851, App
10	60	7.8	428	US-10-196-749-514	Sequence 514, App
11	59.5	7.8	734	US-10-196-749-458	Sequence 458, App
12	59	7.7	702	US-10-538-066-363	Sequence 363, App
13	59	7.7	2026	US-10-505-928-831	Sequence 831, App
14	58.5	7.6	663	US-11-169-140-14	Sequence 14, App
15	58.5	7.6	4590	US-10-505-928-569	Sequence 569, App
16	58	7.6	564	US-10-511-937-2557	Sequence 2557, App
17	58	7.6	730	US-10-505-928-841	Sequence 841, App
18	58	7.6	1645	US-10-505-928-581	Sequence 581, App
19	58	7.6	2413	US-10-511-937-2616	Sequence 2616, App
20	57.5	7.5	980	US-11-242-505A-36	Sequence 36, App
21	57	7.4	635	US-10-511-937-2424	Sequence 2424, App
22	57	7.4	720	US-10-505-928-383	Sequence 383, App
23	56.5	7.4	400	US-11-183-218-46	Sequence 46, App
24	56.5	7.4	558	US-11-311-754-31	Sequence 31, App
25	56.5	7.4	678	US-10-196-749-150	Sequence 150, App

26	56.5	7.4	678	US-11-101-316-34	Sequence 34, App
27	56.5	7.4	5738	US-10-505-928-150	Sequence 150, App
28	56	7.3	140	US-10-468-193-11	Sequence 11, App
29	56	7.3	341	US-10-196-749-224	Sequence 224, App
30	56	7.3	453	US-10-196-749-64	Sequence 64, App
31	56	7.3	541	US-10-468-193-26	Sequence 26, App
32	56	7.3	3256	US-10-505-928-357	Sequence 357, App
33	55.5	7.2	325	US-10-196-749-238	Sequence 238, App
34	55.5	7.2	325	US-11-101-316-64	Sequence 64, App
35	55.5	7.2	524	US-10-918-905-2	Sequence 2, App
36	55.5	7.2	538	US-11-246-999-138	Sequence 138, App
37	55.5	7.2	919	US-11-251-465-31	Sequence 31, App
38	55	7.2	307	US-11-167-773-55	Sequence 55, App
39	55	7.2	307	US-11-167-773-74	Sequence 74, App
40	55	7.2	307	US-10-733-816-6	Sequence 6, App
41	55	7.2	387	US-10-733-816-6	Sequence 6, App
42	55	7.2	461	US-10-511-937-2945	Sequence 2945, App
43	55	7.2	461	US-11-183-218-32	Sequence 32, App
44	55	7.2	473	US-10-505-928-133	Sequence 133, App
45	55	7.2	483	US-10-733-816-4	Sequence 4, App

ALIGNMENTS

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RESULT 1
US-10-505-928-391
; Sequence 391, Application US/10505928
; Publication No. US2006008652A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 391
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-391

Query Match      8.4%; Score 64.5; DB 6; Length 356;
Best Local Similarity 35.8%; Pred. No. 5.1;
Matches 19; Conservative 8; Mismatches 17; Indels 9; Gaps 4;

QY      60 PPSNGVLRAPADGATAMPEKKNKCGTQCPNSQSLSGP--LTQKONGLTWTTTA 110
DB      225 PULPGVL-PAPPDG---PEER---GHSPEPSVVGPGQGVTSMPSSMMSGCA 270

RESULT 2
US-10-511-937-2428
; Sequence 2428, Application US/10511937
; Publication No. US20060086836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
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; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2428
; LENGTH: 413
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-511-937-2428

Query Match
Best Local Similarity 24.4%; Score 64.5; DB 6; Length 413;
Matches 23; Conservative 12; Mismatches 25; Indels 35; Gaps 4;

QY 63 NGVLRPAAPGGINPEKKN---NCGTQCPNSQSL-----SSG-----96
DB 235 NGGNRP-----LIRPKKRLIVSRAGTQCTNCTTTTLMRRNAGDPVPCNACGLYYKCH 289
QY 97 ----PLTOKONGIMTTEAKRDAKMSAREVAISVT 127
DB 290 QVNRPLTMRKDGICTNRRKASGKGGKRGSSLGCT 324

RESULT 3
US-10-370-959-131
; Sequence 131, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Teal, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863, AND
; TITLE OF INVENTION: 32252 MOLECULES AND USBS THEREFOR
; FILE REFERENCE: MP103-0170NMIM
; CURRENT APPLICATION NUMBER: US/10/370,959
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 262
; TYPE: PR
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-370-959-131

Query Match
Best Local Similarity 24.7%; Score 64; DB 6; Length 262;
Matches 20; Conservative 9; Mismatches 32; Indels 20; Gaps 2;

QY 70 APGCIANP-----EKTK-----NCGTQCPNSQSLSSGPTLTKONGIMTTR 109
DB 95 APBARGNPQVLVEKSLGPKHIEYGLADAHNQCITLCNRBCSDQKGINRTQKSIENVASQ 154
QY 110 ARDARMSAREVAISVTENT 130
DB 155 TLTDERQMLREAAVIAHIV 175

RESULT 4
US-11-301-554-1812
; Sequence 1812, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvyck, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; PRIOR FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1812
; LENGTH: 474
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-301-554-1812

Query Match
Best Local Similarity 24.5%; Score 64; DB 7; Length 474;
Matches 26; Conservative 7; Mismatches 27; Indels 46; Gaps 3;
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Qy 27 WLTYDSDALP-----SAAIDSGP----- 46
Db 97 WKLKDSKIPFIREAEERLRKHMADYDYKTRPKRYKSGNANSSSSAAASKEKGD 156
Qy 47 ----EAGGIHAGVLEDGPPSSNGVLRPAAPGIAN--PEKKNCGTO 86
Db 157 KVGSGGGGGGGGGGGSSNAGGGGGGASGGANSEKPAQKSCSK 202

RESULT 5

US-10-511-937-2464
; Sequence 2464, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2464
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2464

Query Match 8.3%; Score 63.5; DB 6; Length 443;
Best Local Similarity 20.8%; Pred. No. 8.9;
Matches 20; Conservative 16; Mismatches 25; Indels 35; Gaps 3;

Qy 63 NGVLRPAAPGIANPEKKMN-----CGTQCPNSOSLS----- 94
Db 294 NGQRP-----LIPKRLSARRAGTSCANCOTTITTLWFRNANGDPVCNACGLYTKLH 348
Qy 95 --SGPLTOKONGLWTTTEAKRDAKMSAREVAISYTE 128
Db 349 NINRPLTMKEGICTRRNRKMSKSKCKKXVHDSLED 384

RESULT 6

US-10-505-928-784
; Sequence 784, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 784
; LENGTH: 2671
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-505-928-784

Query Match 8.1%; Score 62; DB 6; Length 2671;
Best Local Similarity 29.3%; Pred. No. 1.5e+02;
Matches 27; Conservative 16; Mismatches 33; Indels 16; Gaps 7;

Qy 54 GVLEDGSSNGVLRPAAPGIANPEKKM-NGTQ--CP--NSQSLSGPTLQNGLWTTTEA 110
Db 30 GLVVD-----RCVPEPA--GLDNPPEKPRDCLFVPCPNRYS-----AQKQ--YMKAKQ 76
Qy 111 KRDAKMSAREVAISVTENIRQMDRSKRYTKN 142
Db 77 TKQPKKIDVVLQKLGHAQMEKQNDTEN 108

RESULT 7

US-11-251-465-23
; Sequence 23, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-251-465-23

Query Match 8.0%; Score 61.5; DB 7; Length 404;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 28; Conservative 11; Mismatches 42; Indels 17; Gaps 5;

Qy 42 TDSGPEAGIHAAGVLEDGPPSSNGVLRPAAPGIANPEKKMCGTQCPNSOSLSGPTLOK 101
Db 15 TNGVDKAGGVPRAAPDSDASPPGASDAERDDEPGLQVDC--VVGCDK---SSG-----K 66
Qy 102 QNGLWTTT--AKRDAKMSAREVAISVTENIRQMDRSKR 138
Db 67 HYGVFTECGCKSPFKR-----SIRRNLSYTCRSNR 96

RESULT 8

US-10-322-836-48
; Sequence 48, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48

LENGTH: 1075
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (130)...(130)
OTHER INFORMATION: Xaa = Gln or STOP
FEATURE:
NAME/KEY: SITE
LOCATION: (179)...(179)
OTHER INFORMATION: Xaa = Ser or Gly
US-10-322-836-48

Query Match 8.0%; Score 61.5; DB 6; Length 1075;
Best Local Similarity 23.9%; Pred. No. 49;
Matches 27; Conservative 15; Mismatches 52; Indels 19; Gaps 3;

QY 34 DALPSAATSGPAGGLHAGVLEDDGSSNGVLRPAAPGIANPEKMGCTGCPNSQSL 93
DB 860 DTPPRAACSSPHKIPITRGRIE-SPEKRMATFGSAGSINYPDKK-----AL 907

QY 94 SSGPLTKQNGLTTEAKRDARMSAREVAISYTE-----NIRQDRSKRV 139
DB 908 SEGHSMRSTGSTRHSLGDHKSLEALALADIEKTMSTALHELRERQTV 960

RESULT 9

US-10-505-928-851
Sequence 851, Application US/10505928
Publication No. US20060086532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 851
LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-851

Query Match 7.9%; Score 60.5; DB 6; Length 353;
Best Local Similarity 29.1%; Pred. No. 14;
Matches 25; Conservative 12; Mismatches 32; Indels 17; Gaps 4;

QY 37 PSAAATSGPAGGLHAGVLEDDGSSNGVLRPAAPGIA--NPEKMG 83
DB 8 PSEHHEARPMAS---AMSTFAGPSRDSRAMPDAGNHTLAQTASPDTEFGHSGCNSA 64

QY 84 GTCCPNSQSLSGGLTKQNGLTTE 109
DB 65 GVSTPTGSMCP-FOQAQEVGPTWTE 89

RESULT 10
US-10-196-749-514
Sequence 514, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gueney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196,749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 514
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-10-196-749-514

Query Match 7.8%; Score 60; DB 6; Length 428;
Best Local Similarity 19.3%; Pred. No. 20;
Matches 31; Conservative 29; Mismatches 79; Indels 22; Gaps 4;

QY 2 GCCGSRADAIIPPYYSTWRETESWL-TYTDSDALPSAATDSGPAGGLHAGVLEDDG 60
DB 87 GRPPLDTDLHAGSELRVYQTSQTSWTSCTNRMAISSGYS-----TGLGLDKRRGP 141

QY 61 SSNG--VLRPAAPGIANPEKMGCTGCPNSQSLSGGLTKQNGLTTEAKRDKR- 116
DB 142 ASHCQLTSSSTWSEDRPQAVSGHTQCEKADIAPOQTLRLRNDSTSEASRSTHK 201

QY 117 -----MSAREVAISVTENIRQMDRSKRVTKNCIN 145
DB 202 FPLPRRGEPLMLPPLELGYRVTVEDLDREKAAFORIN 242

RESULT 11
US-10-196-749-458
Sequence 458, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gueney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196,749
CURRENT FILING DATE: 2002-07-16

[illegible]

```

RESULT 14
US-11-169-140-14
; Sequence 14, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou. L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLAYNE, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS
; TITLE OF INVENTION: BARRIERS
; FILE REFERENCE: 11474-037-999
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0

```

SEQ ID NO 14
LENGTH: 663
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-11-169-140-14

Query Match 7.6%; Score 58.5; DB 7; Length 663;
Best Local Similarity 24.0%; Pred. No. 54;
Matches 18; Conservative 11; Mismatches 31; Indels 15; Gaps 1;

QY 38 SAATSGPEAGLHAGVLEDEGSSNGVLRPAAPGGIANPEKMGCTGCPNSQSLSSGP 97
DB 211 NVATSDQGRKGRKGV-----PGLATPDKKENDAKSSDSSVGEETLP 255

QY 98 LFOKONGLWTTBAKR 112
DB 256 SSSLKSGKKVAEAK 270

RESULT 15

US-10-505-928-569
Sequence 569, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 569
LENGTH: 4590
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-569

Query Match 7.6%; Score 58.5; DB 6; Length 4590;
Best Local Similarity 21.6%; Pred. No. 7.4e+02;
Matches 27; Conservative 23; Mismatches 56; Indels 19; Gaps 5;

QY 22 ETEST--MLTY--TSDALPSAA-----ATDSCPEAGG--LHAGVLEDEGSSNG 64

DB 1098 DRESTSHYMLTVPATDQGVPLSSFIETIYEVEDVNDNAFQTSEPVYYPEIMENSPKDV 1157

QY 65 VLRPAAPGGIANPEKMGCTGCPNSQSLSSGPLPTOKONGLWTTBAKRDAKMSAREVAI 124

DB 1158 VVQIEAFDPDSSNDKLMYKITSGNPGFPS--IHPKTGLITTSRKLDREODEHILEV 1215

QY 125 SVTEN 129

DB 1216 TVTDN 1220

Search completed: May 20, 2006, 21:23:46
Job time : 5 secs

GenCore version 5.1.8
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OM protein - protein search, using SW model

Run on: May 20, 2006, 21:06:32 ; Search time 38 Seconds
(without alignments)
367.143 Million cell updates/sec

Title: US-10-705-716a-2
Sequence: 1 MGCGSGRADAIERPRTYSWT.....VTENIRQMDRSKRVTKNCIN 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	92.5	12.1	571	T43456	hypothetical prote
2	92.5	12.1	778	A35970	erythrocyte-bindin
3	88	11.5	365	GNVSSC	genome polypeptid
4	83	10.8	1433	S54587	CAT8 protein - yea
5	81	10.6	269	T37073	hypothetical prote
6	79.5	10.4	967	S66852	hypothetical prote
7	78.5	10.4	2559	T09144	probable guanine p
8	78.5	10.2	1199	A40670	nuclear envelope p
9	78	10.2	885	T09225	A kinase anchor pr
10	76.5	10.2	3488	T34418	hypothetical prote
11	76.5	10.0	600	C69899	conserved hypochet
12	76	9.9	645	S19156	serotonin receptor
13	76	9.9	839	E84824	hypothetical prote
14	75.5	9.8	1063	S22571	integrin-like prote
15	75.5	9.8	1122	T47424	bifocal protein -
16	75.5	9.8	368	TVMSUL	transforming prote
17	75	9.8	521	I51633	XPolycarb - Africa
18	74.5	9.7	601	AH0784	probable transpor
19	74.5	9.7	4957	T03455	AKR protein - huma
20	74.5	9.7	5262	T03454	AKR protein - huma
21	74.5	9.6	260	B38584	tropomycin I - fruit
22	74	9.6	742	T38001	probable phosphati
23	74	9.6	832	T31878	hypothetical prote
24	74	9.6	962	T00262	hypothetical prote
25	73.5	9.6	876	A57988	regulatory protein
26	73.5	9.6	960	T37916	probable heterochr
27	73.5	9.6	1575	S68448	synaptonemin, 170K
28	73.5	9.5	403	H98327	enantiomer-selecti

30	73	9.5	453	AE2955	glutanyl-tRNA amid
31	73	9.5	781	T41551	hypothetical prote
32	73	9.5	1274	T37193	enamelin matrix pr
33	72.5	9.5	251	C75521	cytochrome-related
34	72.5	9.5	284	151172	transcription fact
35	72.5	9.5	435	AG1028	prepilin (imported
36	72.5	9.5	503	T35053	probable solute-bi
37	72.5	9.5	516	JB0301	inulinase (EC 3.2.
38	72.5	9.5	1343	AF0611	cell division prot
39	72.5	9.5	3623	T08618	intrinsic factor-B
40	72.5	9.5	5327	T13564	microtubule-associ
41	72	9.4	108	T31565	hypothetical prote
42	72	9.4	1038	JC5757	DNA-directed DNA p
43	72	9.4	1038	T18222	DNA polymerase del
44	72	9.4	1573	T50113	3-dehydroquinone s
45	71.5	9.3	381	AB3048	8-amino-7-oxononan

ALIGNMENTS

RESULT 1
T43456
hypothetical protein DKFZp434L061.1 - human
C/Species: Homo sapiens (man)
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43456
R/Pousska, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A/Reference number: Z22516
A/Accession: T43456
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-571 <AAA>
A/Cross-references: UNIPROT:O75175; UNIPARC:UPI000006FEE9; EMBL:AL133647
A/Experimental source: adult testis; clone DKFZp434L061
C/Genetics:
A/Note: DKFZp434L061.1
C/Superfamily: hydroxyproline-rich glycoprotein

Query Match 12.1%; Score 92.5; DB 2; Length 571;
Best Local Similarity 31.9%; Pred. No. 0.92; Mismatches 32; Indels 25; Gaps 3;
Matches 30; Conservative 7;

QY 31 TDSDALPSAATSGPEAGGSH-----AGVLBDGSPSGVLRPAAP-- 71
Db 111 TDSVSGSPAKNSKQVHSHQPSRAVPPTYSGGPPAASALSTTGNNGVPAAPPS 170

QY 72 --GGIANPEKQKNGTQCPSNGSL---SGPLT 99
Db 171 ALPDKASPAFNSHSGTPAPYAVQAVAPAPSGPST 204

RESULT 2
A35970
erythrocyte-binding protein - Plasmodium knowlesi
C/Species: Plasmodium knowlesi
C/Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C/Accession: A35970
R/Adams, J.H.; Hudson, D.B.; Torii, M.; Ward, G.E.; Wellms, T.E.; Aikawa, M.; Miller, Cell 63, 141-153, 1990
A/Title: The Duffy receptor family of plasmodium knowlesi is located within the micron
A/Reference number: A35970; MUID:91004213; PMID:2170017
A/Accession: A35970
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-778 <ADA>
A/Cross-references: UNIPROT:P22545; UNIPARC:UPI000016BPA8; GB:M68518; GB:M37513; NID:GJ
C/Keywords: transmembrane protein

Query Match 12.1%; Score 92.5; DB 2; Length 778;
Best Local Similarity 33.0%; Pred. No. 1.3; Mismatches 44; Indels 3; Gaps 3;
Matches 29; Conservative 12;

QY 31 TDSALPAAATDSGPAGGIAHAGVLEDEGSSNGV-LRPAAPGIANPEKKNMG-CGQCP 88
 DB 352 TVSSDVPVSGKSGPSTASHALAGENGVEVHNTDTEPKEDGKADPOKIDIVKQKQDR 411
 QY 89 NSGSLSS-GPLTOKONGLMTTEAKRDAK 115
 DB 412 DNRSGSLGPHTRERATLTGETHMEKDTYE 439

RESULT 3

GNVSSC

genome polyprotein - sugarcane mosaic virus (strain SC) (fragment)
 N/Contains: carboxyl end of nuclear inclusion protein b; coat protein
 C/Species: sugarcane mosaic virus, SCMV
 C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C/Accession: PH0207
 R/Frenkel, M.J.; Jilka, J.M.; McKern, N.M.; Strike, P.M.; Clark Jr., J.M.; Shukla, D.D.;
 J. Gen. Virol. 72, 237-242, 1991
 A/Title: Unexpected sequence diversity in the amino-terminal ends of the coat proteins c
 A/Reference number: PH0207; PMID:9113216; PMID:1993866
 A/Accession: PH0207
 A/Molecule type: genomic RNA
 A/Residues: 1-365 <PRE>
 A/Cross-references: UNIPROT:P25242; UNIPARC:UPI0000131E72; GB:D00948; NID:G222123; P1DN:
 C/Superfamily: tobacco etch virus genome polyprotein
 C/Keywords: coat protein; inclusion protein b (fragment) #status predicted <IPB>
 F/1-52/Product: nuclear inclusion protein b (fragment)
 F/53-365/Product: coat protein #status predicted <COA>

Query Match 11.5%; Score 88; DB 1; Length 365;
 Best Local Similarity 21.6%; Pred. No. 1.4;
 Matches 30; Conservative 24; Mismatches 79; Indels 6; Gaps 4;
 QY 5 GSRADATPEPRYESTSTWLTYSDDALPSAAATDSGPAGGIAHAGVLE-EDPSS 62
 DB 21 GIGEEBIE-KYFKPAKDLPGYLEEDYND-EVFNAGVVDAGAGGAGNAGTQPPATAAA 78
 QY 63 NGVLRPAAPGIANPEKKNMGCTGCPNSQSLSGPLTOKONGLMTTEAKRDAKMSAREV 122
 DB 79 GGGAGPPATGAAAPPTTG--GSGLPFGGATGGGAGTGAAGTGSVVGGRDKVDAGTT 136
 QY 123 AISTVTNIRQMDRSKRVTK 141
 DB 137 GKITVPRKAKMSKMRLPK 155

RESULT 4

S54587

CAR8 protein - yeast (Saccharomyces cerevisiae)
 N/Alternate names: MSP8 protein; protein YMR021.06c; protein YMR280C
 C/Species: Saccharomyces cerevisiae
 C/Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004
 C/Accession: S54587; S48234; S61595; S49498
 R/Pearson, D.; Bowman, S.
 submitted to the EMBL Data Library, May 1995
 A/Reference number: S54582
 A/Accession: S54587
 A/Molecule type: DNA
 A/Residues: 1-1433 <PEA>
 A/Cross-references: UNIPROT:P31113; UNIPARC:UPI0000127044; EMBL:Z49704; NID:G825540; P1D:
 R/Experimental source: strain AB972
 R/Grzesitz, D.
 submitted to the EMBL Data Library, March 1994
 A/Reference number: S48234
 A/Accession: S48234
 A/Molecule type: DNA
 A/Residues: 1-746; 'L', 748-1433 <GRZ>
 A/Cross-references: UNIPARC:UPI0000166B45; EMBL:X78344; NID:G559523; P1DN:CAA55139.1; P1:
 R/Boles, B.; Heltmann, C.; Zimmermann, F.K.
 submitted to the EMBL Data Library, December 1995
 A/Reference number: S61594
 A/Accession: S61595

A/Molecule type: DNA
 A/Residues: 1-302; 'A', 304-767; 'A', 769-998; 1003-1007; 'S', 1009-1015; 'Q', 1017-1018; 'P', 102
 A/Cross-references: UNIPARC:UPI0000168D0C; EMBL:X34215; NID:G1122900; P1DN:CAA63906.1;
 A/Experimental source: strain ENY.WA-1A
 C/Genetics:
 A/Gene: SGD:CAT8; MSP8
 A/Cross-references: SGD:S0004893; MIPS:YMR280C
 A/Map position: 13R
 C/Keywords: transmembrane protein
 F/65-102/Domain: GAL4 zinc binuclear cluster homology <GAL4>
 F/456-472/Domain: transmembrane #status predicted <TM1>
 F/738-754/Domain: transmembrane #status predicted <TM2>

Query Match 10.8%; Score 83; DB 2; Length 1433;
 Best Local Similarity 29.4%; Pred. No. 20;
 Matches 32; Conservative 15; Mismatches 50; Indels 12; Gaps 4;
 QY 36 LPAAATDSGPAGGIAHAGVLEDEGSSNGVLRPAAPGIANPEKKNMGCTGCPNSQSLSS 95
 DB 927 LPATTTSKLPLFGSGSKSLERKQRTPVYK-----ENPHEVLYGDSNNNSSEA 979
 QY 96 G--PLTOKONGLMTTEAKRDAKMSAREVAISTENIR--QMDRSKRV 140
 DB 980 GHSPTMTNTNGNRLKYERDAKR-NAKDGISKGENAHNFDNTKQMS 1027

RESULT 5

T37073

hypothetical protein SCJ30.06c - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T37073
 R/Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
 submitted to the EMBL Data Library, August 1999
 A/Reference number: Z21621
 A/Accession: T37073
 A/Status: preliminary; translated from GB/EMBL/DDJ
 A/Molecule type: DNA
 A/Residues: 1-269 <SAN>
 A/Cross-references: UNIPROT:Q9S1Y3; UNIPARC:UPI00000DC600; EMBL:AL109973; P1DN:CA853301
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: SCOEDB:SCJ30.06c

Query Match 10.6%; Score 81; DB 2; Length 269;
 Best Local Similarity 26.8%; Pred. No. 4.5;
 Matches 26; Conservative 9; Mismatches 38; Indels 24; Gaps 4;

QY 11 IEPRYESTW-----RETSTWLTYSDDALPSAAATDSGPAGGIAHAGVLEDP 60
 DB 176 LPETHVEQVVPVNFHCRPRRLVRSGLTTPSPPTVLPSSRCGSGGERTG----- 225
 QY 61 SSGVLRPAAPGIANPEKKNMG--TQCPNSQSLSS 95
 DB 226 -GGGVTTGAGGIV-PGRACRCGRAAHAPTNAMMS 260

RESULT 6

S66852

hypothetical protein YOL155c - yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein O0419; protein MOF1001
 C/Species: Saccharomyces cerevisiae
 C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S66852; S66854; S67325; S70380
 R/Airino, J.; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas,
 submitted to the Protein Sequence Database, July 1996
 A/Reference number: S66814
 A/Accession: S66852
 A/Molecule type: DNA
 A/Residues: 1-967 <ARI>
 A/Cross-references: UNIPROT:Q08294; UNIPARC:UPI000006C5C2; EMBL:Z74897; NID:G1420063; F
 R/Gallion, L.; Dujon, B.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66854
A:Accession: S66854

A:Molecule type: DNA

A:Residues: 1-967 <GAI>

A:Cross-references: UNIPARC:UPI000006C5C2; EMBL:Z74897; NID:g1420063; PIR:e251930; PID:g1420063

A:Experimental source: strain S288C

R:Name, F.J.; Lafuente, M.J.; Casamayor, A.; Aldea, M.; Casaa, C.; Arto, J.; Herrero, E.

submitted to the EMBL Data Library, July 1995

A:Description: Analysis of the DNA sequence of a 1550 bp fragment of the left arm of chromosome III.

A:Reference number: S67324
A:Accession: S67324

A:Molecule type: DNA

A:Residues: 1-164, 'STSTTGGSSATSGSSVSGSSTGATSGSSASGS', 166-186, 'V', 188-967 <GAM>

A:Cross-references: UNIPARC:UPI0000069FE4; EMBL:X89715; NID:g1177620; PID:e190152; PID:g1177620

R:Name, F.J.; Lafuente, M.J.; Casamayor, A.; Arino, J.; Aldea, M.; Casaa, C.; Herrero, E.

Yeast 12, 709-714, 1996

A>Title: Analysis of the DNA sequence of a 15,500 bp fragment near the left telomere of chromosome III.

A:Reference number: S70379; MUID:96405919; PMID:8810044

A:Accession: S70380

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 55-164, 'STSTTGGSSATSGSSVSGSSTGATSGSSASGS', 166-186, 'V', 188-286; 745-773; 781-800

A:Cross-references: UNIPARC:UPI000017CCC3; UNIPARC:UPI000017CCC4; UNIPARC:UPI000017CC5; UNIPARC:UPI000017CC6

C:Genetics:

A:Cross-references: SGD:S0005515

A:Map position: 15L

A>Note: YOL155C

Query Match 10.6%; Score 81; DB 2; Length 967;
Best Local Similarity 24.8%; Pred. No. 20;
Matches 29; Conservativity 23; Mismatches 55; Indels 10; Gaps 2;

Oy 17 ESWRTETSTLTITDSDLPAAATDSGPACG---IHAGVLEDGSSNGVLRPAPG 72
Db 182 RSGSSASGSSSSATSGSSSVSGSSSATSGSSSVSGSSATSGSSASVPSSSGSVTESGSS 241

Oy 73 GIANPEKMGCGTCOPNSQSLSCGPLTKONGLTWTEAKRPAKMSREVIVSTEN 129
Db 242 SSABESSITTOGTGASGSSASTGSSVTGSSSVSGSSAS-----SAPGISSTIPQS 292

RESULT 7
T09144
probable guanine nucleotide exchange factor Rhogef2 - fruit fly (*Drosophila melanogaster*)
N:Alternate names: Shar pel/DRHGF2
C:Species: *Drosophila melanogaster*
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09144; T09223
R:Haecker, U.; Perrimon, N.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z16586
A:Accession: T09144
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2559 <NAE>
A:Cross-references: UNIPROT:O44113; UNIPARC:UPI0000076684; EMBL:AFO31930; NID:g2687355; R:Barrett, K.; Lepplin, M.; Settleman, J.
Cell 91, 905-915, 1997
A>Title: The Rho GTPase and a putative rhoGEF mediate a signaling pathway for the cell cycle.
A:Reference number: Z16618; MUID:98088790; PMID:9428514
A:Accession: T09223
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-676, 'L', 678-837, 'L', 839-889, 'S', 891-1243, 'D', 1245-1358, 'E', 1360-1368, 'R', 1370-1378, 'L', 1380-1387, 'L', 1389-1396, 'L', 1398-1405, 'L', 1407-1414, 'L', 1416-1423, 'L', 1425-1432, 'L', 1434-1441, 'L', 1443-1450, 'L', 1452-1459, 'L', 1461-1468, 'L', 1470-1477, 'L', 1479-1486, 'L', 1488-1495, 'L', 1497-1504, 'L', 1506-1513, 'L', 1515-1522, 'L', 1524-1531, 'L', 1533-1540, 'L', 1542-1549, 'L', 1551-1558, 'L', 1560-1567, 'L', 1569-1576, 'L', 1578-1585, 'L', 1587-1594, 'L', 1596-1603, 'L', 1605-1612, 'L', 1614-1621, 'L', 1623-1630, 'L', 1632-1639, 'L', 1641-1648, 'L', 1650-1657, 'L', 1659-1666, 'L', 1668-1675, 'L', 1677-1684, 'L', 1686-1693, 'L', 1695-1702, 'L', 1704-1711, 'L', 1713-1720, 'L', 1722-1729, 'L', 1731-1738, 'L', 1740-1747, 'L', 1749-1756, 'L', 1758-1765, 'L', 1767-1774, 'L', 1776-1783, 'L', 1785-1792, 'L', 1794-1801, 'L', 1803-1810, 'L', 1812-1819, 'L', 1821-1828, 'L', 1830-1837, 'L', 1839-1846, 'L', 1848-1855, 'L', 1857-1864, 'L', 1866-1873, 'L', 1875-1882, 'L', 1884-1891, 'L', 1893-1900, 'L', 1902-1909, 'L', 1911-1918, 'L', 1920-1927, 'L', 1929-1936, 'L', 1938-1945, 'L', 1947-1954, 'L', 1956-1963, 'L', 1965-1972, 'L', 1974-1981, 'L', 1983-1990, 'L', 1992-1999, 'L', 2001-2008, 'L', 2010-2017, 'L', 2019-2026, 'L', 2028-2035, 'L', 2037-2044, 'L', 2046-2053, 'L', 2055-2062, 'L', 2064-2071, 'L', 2073-2080, 'L', 2082-2089, 'L', 2091-2098, 'L', 2100-2107, 'L', 2109-2116, 'L', 2118-2125, 'L', 2127-2134, 'L', 2136-2143, 'L', 2145-2152, 'L', 2154-2161, 'L', 2163-2170, 'L', 2172-2179, 'L', 2181-2188, 'L', 2190-2197, 'L', 2199-2206, 'L', 2208-2215, 'L', 2217-2224, 'L', 2226-2233, 'L', 2235-2242, 'L', 2244-2251, 'L', 2253-2260, 'L', 2262-2269, 'L', 2271-2278, 'L', 2280-2287, 'L', 2289-2296, 'L', 2298-2305, 'L', 2307-2314, 'L', 2316-2323, 'L', 2325-2332, 'L', 2334-2341, 'L', 2343-2350, 'L', 2352-2359, 'L', 2361-2368, 'L', 2370-2377, 'L', 2379-2386, 'L', 2388-2395, 'L', 2397-2404, 'L', 2406-2413, 'L', 2415-2422, 'L', 2424-2431, 'L', 2433-2440, 'L', 2442-2449, 'L', 2451-2458, 'L', 2460-2467, 'L', 2469-2476, 'L', 2478-2485, 'L', 2487-2494, 'L', 2496-2503, 'L', 2505-2512, 'L', 2514-2521, 'L', 2523-2530, 'L', 2532-2539, 'L', 2541-2548, 'L', 2550-2557, 'L', 2559-2566, 'L', 2568-2575, 'L', 2577-2584, 'L', 2586-2593, 'L', 2595-2602, 'L', 2604-2611, 'L', 2613-2620, 'L', 2622-2629, 'L', 2631-2638, 'L', 2640-2647, 'L', 2649-2656, 'L', 2658-2665, 'L', 2667-2674, 'L', 2676-2683, 'L', 2685-2692, 'L', 2694-2701, 'L', 2703-2710, 'L', 2712-2719, 'L', 2721-2728, 'L', 2730-2737, 'L', 2739-2746, 'L', 2748-2755, 'L', 2757-2764, 'L', 2766-2773, 'L', 2775-2782, 'L', 2784-2791, 'L', 2793-2800, 'L', 2802-2809, 'L', 2811-2818, 'L', 2820-2827, 'L', 2829-2836, 'L', 2838-2845, 'L', 2847-2854, 'L', 2856-2863, 'L', 2865-2872, 'L', 2874-2881, 'L', 2883-2890, 'L', 2892-2899, 'L', 2901-2908, 'L', 2910-2917, 'L', 2919-2926, 'L', 2928-2935, 'L', 2937-2944, 'L', 2946-2953, 'L', 2955-2962, 'L', 2964-2971, 'L', 2973-2980, 'L', 2982-2989, 'L', 2991-2998, 'L', 2999-3006, 'L', 3007

C/Function: mediates actin rearrangements required for cell shape changes during ga
C/Superfamily: rat Munc13-3 protein, protein kinase C zinc-binding repeat homology
C/Keywords: embryo, GTP exchange, signal transduction
P1151-1200/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 10.4%; Score 79.5; DB 2; Length 2559;
Best Local Similarity 28.3%; Pred. No. 83;
Matches 30; Conservative 11; Mismatches 56; Indels 9; Gaps 3;

QY 5 GSRDAIEPRYESWTRETSTWLTYYTSDALPSAAATDGPBAGLHAGVLEDPSSNG 64
DB 799 GSSPNNMPPRHPRDRITKTTSGSW-EIVEKDGSSPPGTPPPYLSSSHMTVLEDPENNRR 857
QY 65 VLRPAAPG-GIANPEKKNCGQCPSNOSLSGGP-----TOKQ 102
DB 858 GAAAGGVTFIESHOFTPMAGASSPIPLSHNMHMAAQSNDTQKE 903

RESULT 8
A40670
nuclear envelope protein POM 121 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: A40670
R/Hallberg, E.; Moznjak, R.W.; Blobel, G.
J. Cell Biol. 122, 513-521, 1993
A>Title: An integral membrane protein of the pore membrane domain of the nuclear envel
A/Reference number: A40670; MUID:93328754; PMID:8335683
A/Accession: A40670
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-1199 <HML>
A/Cross-references: UNIPROT:P52591; UNIPARC:UPI000012FCOE; GB:Z21513; NID:9396746; PID:
F:803-807,845-849,956-960,1010-1047,1047-1051,1076-1080/Region: pentapeptide motif (X-
Query Match 10.2%; Score 78.5; DB 2; Length 1199;
Best Local Similarity 25.2%; Pred. No. 43;
Matches 39; Conservative 19; Mismatches 56; Indels 41; Gaps 6;

QY 20 TRETESTWLTYYTSDALPSA---AATDGPBAGLHAGVLEDPSSNGVLRPAAPGIA- 75
DB 363 SRTSSVSLITCTCGGIRSSRNAITSSYSTRGVSQLMKSGPTSSPPSPASHRSQTP 422
QY 76 -NPEKKNCGTQCPSNOSLSGGP-----TOKNGIWT-----EAK 111
DB 423 ERPAAKTR--EBPCHQSSSAPLVTDKSPGEKVTDPATGQGLMTSSPTPGSSGQRK 480
QY 112 RDAKMSAR-----EVALSVTENIKQMDR 135
DB 481 RKIQLPSRRGDQLTPPPPELGYSITAEDDMER 515

RESULT 9
T09225
A/kinase anchor protein AKAP-KL isoform 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T09225; T09226; T09227
R/Dong, F.; Feldmesser, M.; Casadevall, A.; Rubin, C.S.
J. Biol. Chem. 273, 6533-6541, 1998
A>Title: Molecular characterization of a cDNA that encodes six isoforms of a novel murin
A/Reference number: Z16620; MUID:98165844; PMID:9497389
A/Accession: T09225
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-885 <DON>
A/Cross-references: UNIPROT:O54931; UNIPARC:UPI000028356; EMBL:AF033274; NID:62852696
A/Note: binds the regulatory subunits (RII) of protein kinase AII isoforms
A/Accession: T09226
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-848,862-885 <DO2>

Db 489 TTTSERKALSGAGVVAAGVAGSGSGEGAGTGKAGVGLGGLASTANPHOKL---- 545

QY 85 TQCPNSQSLSSGPILOKONGMTTEAKRDARMSAREVAI 124

Db 546 -----AKRRQL-LEAKRE-RKAAQTIAI 566

RESULT 13

884824

hypothetical protein At2g40040 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: B84824

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.E.; Umayam, L.; Tallon, L.

euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617137

A/Accession: B84824

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-839 <STO>

A/Cross-references: UNIPROT:O04207; UNIPARC:UPI00000A862E; GB:AE002093; NID:g2088657; P

C/Genetics:

A/Gene: At2g40040

A/Map position: 2

Query Match 9.8%; Score 76; DB 2; Length 839;

Best Local Similarity 23.8%; Pred. No. 48;

Matches 40; Conservative 14; Mismatches 62; Indels 52; Gaps 6;

QY 5 GSRADAIETPRYSWTR---ETESTWLTYYTSDALPSAAA----- 41

Db 338 GSGAGVIGP-----WNKKSSTESNGATWSSDRTKSGAAMNSWDKNITDSEPAWG 392

QY 42 -----TDSGPAGGL---HAGVLEDPSSNGV-----LRPAAPGIANPEKM 81

Db 393 SGGKNSSETSGPAAWAMDKKSETERGPAWGMGCKKNSSETELGPAAMGMDKKSDT 452

QY 82 NCGQCNSQSLSSGPILOKONGMTTEAKRDARMSAREVAISVTEN 129

Db 453 KSGPAAWGSTDAAWSSSDKKN---SETSDAAMGSRNKKTSIES 496

RESULT 14

S22571

integrase-like protein PE65 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C/Accession: S22571; S22572

R/Diullo, A.; Zambirano, N.; Mogavero, A.R.; Ammendola, R.; Cimino, F.; Russo, T.

Nucleic Acids Res. 19, 5269-5274, 1991

A/Title: A rat brain mRNA encoding a transcriptional activator homologous to the DNA bit

A/Reference number: S22571; MUID:92020215; PMID:1923810

A/Accession: S22571

A/Molecule type: mRNA

A/Residues: 1-499 <DU11>

A/Cross-references: UNIPROT:Q99MK3; UNIPARC:UPI0000170BC8; EMBL:X60469; NID:g57559; PIN

A/Accession: S22572

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 31-318 <DU12>

A/Cross-references: UNIPARC:UPI0000170BC9; EMBL:X60468; NID:g57561; PIN:CAA42998.1; P

A/Note: this sequence was submitted to the EMBL Data Library, July 1991

C/Genetics:

A/Intons: 88/3; 107/3; 135/3; 157/3; 207/3; 250/2; 252/2; 290/3

C/Keywords: transcription regulation

F/42-78/Domain: WW repeat homology <WW1>

Query Match

9.8%; Score 75.5; DB 2; Length 499;

Best Local Similarity 25.6%; Pred. No. 29;

Matches 34; Conservative 17; Mismatches 59; Indels 23; Gaps 5;

QY 13 PRYESWTRFETESTWLTYYTSDALPSAAATDSPEBAGLHAGVLEDPSSNGVLRPAAPG 72

Db 77 PSQNSFQESQQLTWGPF-----AHQEGFEEGEP-----WKDPSERAPMEL----- 118

QY 73 GIANPEKKNCGQCPCNSQSLSSGPILOKONGMTTEAKRDARMSAREVA-ISVTENIR 131

Db 119 GLKDPER---GTLPPSAQSLSPFPVQEBENLPORNANPGICPAVRSLGWMTEBEL 174

QY 132 QMDRSKRVTKNCI 144

Db 175 APGRSSVAVNNCI 187

RESULT 15

T03743

bifocal protein - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C/Accession: T03743

R/Bahr, S.M.; Yang, X.Y.; Chia, W.

Mol. Cell. Biol. 17, 5521-5529, 1997

A/Title: The Drosophila bifocal gene encodes a novel protein which colocalizes with act

A/Reference number: Z15048; MUID:97415628; PMID:9271427

A/Accession: T03743

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-1063 <BAH>

A/Cross-references: UNIPROT:O16125; UNIPARC:UPI000017BE7D; EMBL:AF011791; NID:g238667,

C/Genetics:

A/Cross-references: FlyBase:FBgn0014133

A/Note: bifocal

Query Match 9.8%; Score 75.5; DB 2; Length 1063;

Best Local Similarity 20.7%; Pred. No. 70;

Matches 39; Conservative 23; Mismatches 59; Indels 67; Gaps 6;

QY 5 GSRADAIETPRYSWTR---ETESTWLTYYTSDAL-----PSAAAT- 42

Db 83 GA1ADFTPATISTSQKRWIMGSEKSKSISNTNSDSTGGHSAVASLSPDAATT 142

QY 43 -----DSPEBAGLHAGVLEDPSSNGVLRPAAPG 72

Db 143 NVTVPDIPKORSLNTRSGEREMVRYIIISGSGRDELESGOPAGVVSNSRCGEVETG 202

QY 73 GIANPEKKNCGQCPCNSQSLSSGPILOKONGMTTEAKRDARMSAREVAISVTENIR 132

Db 203 TIGSPSSAN---QNPVPHLK---TKCKPGQSVABGRFSALG-----TIVDSKS 247

QY 133 MDRSKRVT 140

Db 248 CSKTKGIS 255

Search completed: May 20, 2006, 21:07:20
Job time: 40 secs